

SEQUENCE LISTING

<110> O'Donnell, Michael E.

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Bruck, Irina

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<120> ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
USE THEREOF

<130> 22221/1030

<140> 09/716,964

<141> 2000-11-21

<150> 60/143,202

<151> 1997-04-08

<150> 08/823,407

<151> 1997-04-08

<150> 09/057,416

<151> 1998-04-08

<160> 212

<170> PatentIn Ver. 2.1

<210> 1

<211> 2007

<212> DNA

<213> Thermus thermophilus

<400> 1

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<210> 2

<211> 529

<212> PRT

<213> *Thermus thermophilus*

<400> 2

Met Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
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Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
20 25 30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
35 40 45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
50 55 60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
65 70 75 80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
85 90 95

Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 355 360 365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 370 375 380

Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 385 390 395 400

Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 405 410 415

Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 420 425 430

Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
 435 440 445

Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro
 450 455 460

Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Glu Val Glu Ala Glu
 465 470 475 480

Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
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Leu Leu Gly Gly Arg Val Leu Trp Val Arg Arg Pro Arg Thr Arg Glu
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Ala Pro Glu Glu Glu Pro Leu Ser Gln Asp Glu Ile Gly Gly Thr Gly
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<210> 3

<211> 1590

<212> DNA

<213> Thermus thermophilus

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<210> 4

<211> 464

<212> PRT

<213> *Thermus thermophilus*

<400> 4

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Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
      20             25             30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
      35             40             45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
      50             55             60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
      65             70             75             80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
      85             90             95

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Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
 355 360 365

Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
 370 375 380

Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
 385 390 395 400

Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
 405 410 415

Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
 420 425 430

Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
 435 440 445

Gly Glu Lys Lys Lys Pro Glu Pro Lys Ala Pro Pro Gly Pro Thr Ser
 450 455 460

<210> 5

<211> 454

<212> PRT

<213> Thermus thermophilus

<400> 5

Met Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1 5 10 15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20 25 30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser

340	345	350
Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro		
355	360	365
Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe		
370	375	380
Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg		
385	390	400
Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys		
405	410	415
Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro		
420	425	430
Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu		
435	440	445
Gly Glu Lys Lys Lys Ala		
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<210> 6
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 6
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<210> 7
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 7
 His Ala Tyr Leu Phe Ser Gly Thr
 1 5

<210> 8
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 8
 cgcggaattcg tgctcsggsg gctcctcsag sgtc 34

<210> 9
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: peptide

<400> 9
 Lys Thr Leu Glu Glu Pro Pro Glu His
 1 5

<210> 10
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 10
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<210> 11
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 11
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<210> 12
 <211> 28
 <212> DNA
 <213> Artificial Sequence

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 <223> Description of Artificial Sequence: primer

 <400> 12
 gaattaaatt cgcgcttcgg gaggtggg 28

 <210> 13
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 13
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 <210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 14
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 <210> 15
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 15
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<210> 16
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 16
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31

<210> 17
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: peptide

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 <222> (2)
 <223> X is any aa at position 2

 <220>
 <221> PEPTIDE
 <222> (3)
 <223> X is any aa at position 3

 <220>
 <221> PEPTIDE
 <222> (5)
 <223> X is any aa at position 5

 <400> 17
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<210> 18
 <211> 12
 <212> PRT
 <213> Artificial Sequence

 <220>

<223> Description of Artificial Sequence: peptide

<400> 18

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<210> 19

<211> 180

<212> PRT

<213> Escherichia coli

<400> 19

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Val Leu Thr Ala Leu Ala Asn Gly Leu
20 25 30

Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60

Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80

Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110

Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Val
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<210> 20

<211> 180

<212> PRT

<213> Bacillus subtilis

<400> 20

Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
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Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
20 25 30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
50 55 60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys
65 70 75 80

Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala
85 90 95

Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys
100 105 110

Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val
115 120 125

His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His
145 150 155 160

Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys
165 170 175

Arg Ile Thr Ser
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<210> 21

<211> 294

<212> PRT

<213> Escherichia coli

<400> 21

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Gln Thr Phe Ala
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20 25 30
Ser Leu Gly Arg Ile His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45
Val Gly Lys Thr Ser Ile Ala Arg Leu Leu Ala Lys Gly Leu Asn Cys
50 55 60
Glu Thr Gly Ile Thr Ala Thr Pro Cys Gly Val Cys Asp Asn Cys Arg
65 70 75 80
Glu Ile Glu Gln Gly Arg Phe Val Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95
Ser Arg Thr Lys Val Glu Asp Thr Arg Asp Leu Leu Asp Asn Val Gln
100 105 110
Tyr Ala Pro Ala Arg Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125
His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140
Glu Pro Pro Glu His Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160
Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175
Ala Leu Asp Val Glu Gln Ile Arg His Gln Leu Glu His Ile Leu Asn
180 185 190
Glu Glu His Ile Ala His Glu Pro Arg Ala Leu Gln Leu Leu Ala Arg
195 200 205
Ala Ala Glu Gly Ser Leu Arg Asp Ala Leu Ser Leu Thr Asp Gln Ala
210 215 220
Ile Ala Ser Gly Asp Gly Gln Val Ser Thr Gln Ala Val Ser Ala Met
225 230 235 240

Leu Gly Thr Leu Asp Asp Asp Gln Ala Leu Ser Leu Val Glu Ala Met
245 250 255

Val Glu Ala Asn Gly Glu Arg Val Met Ala Leu Ile Asn Glu Ala Ala
260 265 270

Ala Arg Gly Ile Glu Trp Glu Ala Leu Leu Val Glu Met Leu Gly Leu
275 280 285

Leu His Arg Ile Ala Met
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<210> 22

<211> 294

<212> PRT

<213> Haemophilus influenzae

<400> 22

Met Ser Tyr Gln Val Leu Ala Arg Lys Trp Arg Pro Lys Thr Phe Ala
1 5 10 15

Asp Val Val Gly Gln Glu His Ile Ile Thr Ala Leu Ala Asn Gly Leu
20 25 30

Lys Asp Asn Arg Leu His His Ala Tyr Leu Phe Ser Gly Thr Arg Gly
35 40 45

Val Gly Lys Thr Ser Ile Ala Arg Leu Phe Ala Lys Gly Leu Asn Cys
50 55 60

Val His Gly Val Thr Ala Thr Pro Cys Gly Glu Cys Glu Asn Cys Lys
65 70 75 80

Ala Ile Glu Gln Gly Asn Phe Ile Asp Leu Ile Glu Ile Asp Ala Ala
85 90 95

Ser Arg Thr Lys Val Glu Asp Thr Arg Glu Leu Leu Asp Asn Val Gln
100 105 110

Tyr Lys Pro Val Val Gly Arg Phe Lys Val Tyr Leu Ile Asp Glu Val
115 120 125

His Met Leu Ser Arg His Ser Phe Asn Ala Leu Leu Lys Thr Leu Glu
130 135 140

Glu Pro Pro Glu Tyr Val Lys Phe Leu Leu Ala Thr Thr Asp Pro Gln
145 150 155 160

Lys Leu Pro Val Thr Ile Leu Ser Arg Cys Leu Gln Phe His Leu Lys
165 170 175

Ala Leu Asp Glu Thr Gln Ile Ser Gln His Leu Ala His Ile Leu Thr
180 185 190

Gln Glu Asn Ile Pro Phe Glu Asp Pro Ala Leu Val Lys Leu Ala Lys
195 200 205

Ala Ala Gln Gly Ser Ile Arg Asp Ser Leu Ser Leu Thr Asp Gln Ala
210 215 220

Ile Ala Met Gly Asp Arg Gln Val Thr Asn Asn Val Val Ser Asn Met
225 230 235 240

Leu Gly Leu Leu Asp Asp Asn Tyr Ser Val Asp Ile Leu Tyr Ala Leu
245 250 255

His Gln Gly Asn Gly Glu Leu Leu Met Arg Thr Leu Gln Arg Val Ala
260 265 270

Asp Ala Ala Gly Asp Trp Asp Lys Leu Leu Gly Glu Cys Ala Glu Lys
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Leu His Gln Ile Ala Leu
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<210> 23

<211> 294

<212> PRT

<213> Bacillus subtilis

<400> 23

Met Ser Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Glu
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Asp Val Val Gly Gln Glu His Ile Thr Lys Thr Leu Gln Asn Ala Leu
20 25 30

Leu Gln Lys Lys Phe Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
35 40 45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
50 55 60

Glu His Ala Pro Val Asp Glu Pro Cys Asn Glu Cys Ala Ala Cys Lys

65		70		75		80
Gly Ile Thr Asn Gly Ser Ile Ser Asp Val Ile Glu Ile Asp Ala Ala						
- - - - - 85 - - - - - 90 - - - - - 95 - - - - -						
Ser Asn Asn Gly Val Asp Glu Ile Arg Asp Ile Arg Asp Lys Val Lys						
100		105		110		
Phe Ala Pro Ser Ala Val Thr Tyr Lys Val Tyr Ile Ile Asp Glu Val						
115		120		125		
His Met Leu Ser Ile Gly Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu						
130		135		140		
Glu Pro Pro Glu His Cys Ile Phe Ile Leu Ala Thr Thr Glu Pro His						
145		150		155		160
Lys Ile Pro Leu Thr Ile Ile Ser Arg Cys Gln Arg Phe Asp Phe Lys						
165		170		175		
Arg Ile Thr Ser Gln Ala Ile Val Gly Arg Met Asn Lys Ile Val Asp						
180		185		190		
Ala Glu Gln Leu Gln Val Glu Glu Gly Ser Leu Glu Ile Ile Ala Ser						
195		200		205		
Ala Ala His Gly Gly Met Arg Asp Ala Leu Ser Leu Leu Asp Gln Ala						
210		215		220		
Ile Ser Phe Ser Gly Asp Ile Leu Lys Val Glu Asp Ala Leu Leu Ile						
225		230		235		240
Thr Gly Ala Val Ser Gln Leu Tyr Ile Gly Lys Leu Ala Lys Ser Leu						
245		250		255		
His Asp Lys Asn Val Ser Asp Ala Leu Glu Thr Leu Asn Glu Leu Leu						
260		265		270		
Gln Gln Gly Lys Asp Pro Ala Lys Leu Ile Glu Asp Met Ile Phe Tyr						
275		280		285		
Phe Arg Asp Met Leu Leu						
290						

<210> 24
 <211> 300
 <212> PRT

<213> Caulobacter crescentus

<400> 24

Asp-Ala-Tyr Thr Val Leu Ala Arg Lys-Tyr Arg Pro Arg Thr Phe Glu
1 5 10 15

Asp Leu Ile Gly Gln Glu Ala Met Val Arg Thr Leu Ala Asn Ala Phe
20 25 30

Ser Thr Gly Arg Ile Ala His Ala Phe Met Leu Thr Gly Val Arg Gly
35 40 45

Val Gly Lys Thr Thr Thr Ala Arg Leu Leu Ala Arg Ala Leu Asn Tyr
50 55 60

Glu Thr Asp Thr Val Lys Gly Pro Ser Val Asp Leu Thr Thr Glu Gly
65 70 75 80

Tyr His Cys Arg Ser Ile Ile Glu Gly Arg His Met Asp Val Leu Glu
85 90 95

Leu Asp Ala Ala Ser Arg Thr Lys Val Asp Glu Met Arg Glu Leu Leu
100 105 110

Asp Gly Val Arg Tyr Ala Pro Val Glu Ala Arg Tyr Lys Val Tyr Ile
115 120 125

Ile Asp Glu Val His Met Leu Ser Thr Ala Ala Phe Asn Ala Leu Leu
130 135 140

Lys Thr Leu Glu Glu Pro Pro Pro His Ala Lys Phe Ile Phe Ala Thr
145 150 155 160

Thr Glu Ile Arg Lys Val Pro Val Thr Ile Leu Ser Arg Cys Gln Arg
165 170 175

Phe Asp Leu Arg Arg Val Glu Pro Asp Val Leu Val Lys His Phe Asp
180 185 190

Arg Ile Ser Ala Lys Glu Gly Ala Arg Ile Glu Met Asp Ala Leu Ala
195 200 205

Leu Ile Ala Arg Ala Ala Glu Gly Ser Val Arg Asp Gly Leu Ser Leu
210 215 220

Leu Asp Gln Ala Ile Val Gln Thr Glu Arg Gly Gln Thr Val Thr Ser
225 230 235 240

Thr Val Val Arg Asp Met Leu Gly Leu Ala Asp Arg Ser Gln Thr Ile
245 250 255

- Ala Leu Tyr Glu His Val Met Ala Gly Lys Thr Lys Asp Ala-Leu Glu
260 265 270

Gly Phe Arg Ala Leu Trp Gly Phe Gly Ala Asp Pro Ala Val Val Met
275 280 285

Leu Asp Val Leu Asp His Cys His Ala Ser Ala Val
290 295 300

<210> 25

<211> 260

<212> PRT

<213> Mycoplasma genitalium

<400> 25

Met His Gln Val Phe Tyr Gln Lys Tyr Arg Pro Ile Asn Phe Lys Gln
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Thr Leu Gly Gln Glu Ser Ile Arg Lys Ile Leu Val Asn Ala Ile Asn
20 25 30

Arg Asp Lys Leu Pro Asn Gly Tyr Ile Phe Ser Gly Glu Arg Gly Thr
35 40 45

Gly Lys Thr Thr Phe Ala Lys Ile Ile Ala Lys Ala Ile Asn Cys Leu
50 55 60

Asn Trp Asp Gln Ile Asp Val Cys Asn Ser Cys Asp Val Cys Lys Ser
65 70 75 80

Ile Asn Thr Asn Ser Ala Ile Asp Ile Val Glu Ile Asp Ala Ala Ser
85 90 95

Lys Asn Gly Ile Asn Asp Ile Arg Glu Leu Val Glu Asn Val Phe Asn
100 105 110

His Pro Phe Thr Phe Lys Lys Lys Val Tyr Ile Leu Asp Glu Ala His
115 120 125

Met Leu Thr Thr Gln Ser Trp Gly Gly Leu Leu Lys Thr Leu Glu Glu
130 135 140

Ser Pro Pro Tyr Val Leu Phe Ile Phe Thr Thr Thr Glu Phe Asn Lys
145 150 155 160

Ile Pro Leu Thr Ile Leu Ser Arg Cys Gln Ser Phe Phe Phe Lys Lys
 165 170 175

Ile Thr Ser Asp Leu Ile Leu Glu Arg Leu Asn Asp Ile Ala Lys Lys
 180 185 190

Glu Lys Ile Lys Ile Glu Lys Asp Ala Leu Ile Lys Ile Ala Asp Leu
 195 200 205

Ser Gln Gly Ser Leu Arg Asp Gly Leu Ser Leu Leu Asp Gln Leu Ala
 210 215 220

Ile Ser Leu Ile Val Lys Lys Leu Val Leu Leu Met Leu Lys Lys His
 225 230 235 240

Leu Ile Ser Leu Ile Glu Met Gln Asn Leu Leu Leu Leu Lys Gln Phe
 245 250 255

Tyr Gln Glu Ile
 260

<210> 26

<211> 289

<212> PRT

<213> Thermus thermophilus

<400> 26

Val Ser Ala Leu Tyr Arg Arg Phe Arg Pro Leu Thr Phe Gln Glu Val
 1 5 10 15

Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
 20 25 30

Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
 35 40 45

Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
 50 55 60

Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
 65 70 75 80

Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
 85 90 95

Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu

100	105	110
Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser		
115	120	125
Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro		
130	135	140
His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro		
145	150	155
Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu		
165	170	175
Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg		
180	185	190
Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly		
195	200	205
Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu		
210	215	220
Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro		
225	230	235
Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr		
245	250	255
Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala		
260	265	270
Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu		
275	280	285
Tyr		

<210> 27

<211> 94

<212> DNA

<213> Thermus thermophilus

<400> 27

gccggaggga gaaaaaaaaa gccgagccca aggcccccgc	cgccccacc ccgaagcgcc	60
cgcacccccg ggccccccga ggaggaggag aggc		94

<210> 28
<211> 11
<212> PRT
<213> Thermus thermophilus

<400> 28
Val Leu Glu Gly Glu Lys Lys Ser Leu Ser Pro
1 5 10

<210> 29
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (6)
<223> N at position 6 is either G or C

<220>
<221> unsure
<222> (12)
<223> N at position 12 is either G or C

<220>
<221> unsure
<222> (21)
<223> N at position 21 is either G or C

<400> 29
cacgcntacc tnttctccgg nac 23

<210> 30
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure

<222> (7)
<223> N at position 7 is either G or C

... <220>
<221> unsure
<222> (10)
<223> N at position 10 is either G or C

<220>
<221> unsure
<222> (19)
<223> N at position 19 is either G or C

<220>
<221> unsure
<222> (22)
<223> N at position 22 is either G or C

<400> 30
gtgctcnggn ggctcctcnt cngtc 25

<210> 31
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 31
gtgggatccg tggttctgga tctcgatgaa gaa 33

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 32
gtgggatcca cggscststcs gagcagaag 29

<210> 33
<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 33

gcgggatacct caacgaggac ctctccatct tcaa

34

<210> 34

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 34

gcgggatacct tgctgtcsag sgtsagsgcg tcgta

35

<210> 35

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 35

gggaaggacc agcgcgtact cccctgctc ctaggtgtg

39

<210> 36

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 36

gtgtggatcc ttcttcttsc ccatsgc

27

<210> 37

<211> 27

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 37
caccgattcc agtggtgcct aggtgtg

27

<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 38
caacacctgg tgttccagga gcctgtgctt

30

<210> 39
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 39
ccagaatcgt ctgctggtcg tag

23

<210> 40
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 40
agcaccctgg aggagcttc

19

<210> 41
<211> 19

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 41
catgtcgtac tgggtgtac

19

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<220>
<221> unsure
<222> (7)
<223> N at position 7 is A, C, G, or T

<220>
<221> unsure
<222> (8)
<223> N at position 8 is A, C, G, or T

<220>
<221> unsure
<222> (13)
<223> N at position 13 is A, C, G, or T

<220>
<221> unsure
<222> (14)
<223> N at position 14 is A, C, G, or T

<400> 42
gtsqtsnnsq acnnsqagac sacsggg

27

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<220>

<221> unsure

<222> (8)

<223> N at position 8 is A, C, G, or T

<220>

<221> unsure

<222> (9)

<223> N at position 9 is A, C, G, or T

<220>

<221> unsure

<222> (17)

<223> N at position 17 is A, C, G, or T

<220>

<221> unsure

<222> (18)

<223> N at position 18 is A, C, G, or T

<400> 43

gaasccsnng tcgaasnngg cgttgtg

27

<210> 44

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 44

cggggatcca cctcaatcac ctcggtg

27

<210> 45

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 45

cggggatccg ccaccttgcg gctccgggtg

30

<210> 46

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 46

gcgctctaga cgagttccca aagcgtgcgg t

31

<210> 47

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 47

cgcgtctaga tcacctgtat ccaga

25

<210> 48

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 48

gcggcgcata tgggtggtggt cctggacctg gag

33

<210> 49

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 49

cgcgtctaga tcacctgtat ccaga

25

<210> 50
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 50
 gtsctsgtsa agacscactt 20

 <210> 51
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 51
 sagsagsgcg ttgaasgtgt g 21

 <210> 52
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 52
 ctcgttggtg aaagtttccg tg 22

 <210> 53
 <211> 22
 <212> DNA
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 <220>
 <223> Description of Artificial Sequence: primer

 <400> 53
 ctcgttggtg aaagtttccg tg 22

<210> 54
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 54
 tctggcaaca cgttctggag cacatcc 27

 <210> 55
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 55
 tgctggcggt catcttcagg atg 23

 <210> 56
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 56
 catcctgaag atgaacgcca gca 23

 <210> 57
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 57
 aggttatcca caggggtcat gtgca 25

<210> 58
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 58
 gtgtgtcata tgaacataac gggtcccaa 29

<210> 59
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 59
 gcgcgaattc tcccttgtgg aaggcttag 29

<210> 60
 <211> 13
 <212> PRT
 <213> Thermus thermophilus

<400> 60
 Arg Val Glu Leu Asp Tyr Asp Ala Leu Thr Leu Asp Asp
 1 5 10

<210> 61
 <211> 14
 <212> PRT
 <213> Thermus thermophilus

<400> 61
 Phe Phe Ile Glu Ile Gln Asn His Gly Leu Ser Glu Gln Lys
 1 5 10

<210> 62
 <211> 8

<212> PRT
<213> Thermus thermophilus

<400> 62
Phe Phe Ile Glu Ile Gln Asn His
1 5

<210> 63
<211> 8
<212> PRT
<213> Thermus thermophilus

<400> 63
Tyr Asp Ala Leu Thr Leu Asp Asp
1 5

<210> 64
<211> 6
<212> PRT
<213> Thermus thermophilus

<400> 64
Ala Met Gly Lys Lys Lys
1 5

<210> 65
<211> 9
<212> PRT
<213> Thermus thermophilus

<400> 65
Phe Asn Lys Ser His Ser Ala Ala Tyr
1 5

<210> 66
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE

<222> (3)
<223> Xaa at position 3 is undefined

<220>
<221> PEPTIDE
<222> (5)
<223> Xaa at position 5 is undefined

<400> 66
Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 67
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (4)
<223> Xaa at position 4 is undefined

<220>
<221> PEPTIDE
<222> (7)
<223> Xaa at position 7 is undefined

<400> 67
His Asn Ala Xaa Phe Asp Xaa Gly Phe
1 5

<210> 68
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: peptide

<220>
<221> PEPTIDE
<222> (3)
<223> Xaa at position 3 is undefined

<220>

<221> PEPTIDE

<222> (5)

<223> Xaa at position 5 is undefined

<400> 68

Val Val Xaa Asp Xaa Glu Thr Thr Gly
1 5

<210> 69

<211> 7

<212> PRT

<213> Thermus thermophilus

<400> 69

Val Leu Val Lys Thr His Leu
1 5

<210> 70

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide

<400> 70

His Arg Ala Leu Tyr Asp
1 5

<210> 71

<211> 7

<212> PRT

<213> Thermus thermophilus

<400> 71

His Thr Phe Asn Ala Leu Leu
1 5

<210> 72

<211> 34

<212> PRT

<213> Escherichia coli

<400> 72

Asp Arg Tyr Phe Leu Glu Leu Ile Arg Thr Gly Arg Pro Asp Glu Glu

1 - 5 - - - 10 - - - 15 - - - - -

Ser Tyr Leu His Ala Ala Val Glu Leu Ala Glu Ala Arg Gly Leu Pro

20 25 30

Val Val

<210> 73

<211> 34

<212> PRT

<213> *Vibrio cholerae*

<400> 73

Asp His Phe Tyr Leu Glu Leu Ile Arg Thr Gly Arg Ala Asp Glu Glu

1 5 10 15

Ser Tyr Leu His Phe Ala Leu Asp Val Ala Glu Gln Tyr Asp Leu Pro

20 25 30

Val Val

<210> 74

<211> 34

<212> PRT

<213> *Haemophilus influenzae*

<400> 74

Asp His Phe Tyr Leu Ala Leu Ser Arg Thr Gly Arg Pro Asn Glu Glu

1 5 10 15

Arg Tyr Ile Gln Ala Ala Leu Lys Leu Ala Glu Arg Cys Asp Leu Pro

20 25 30

Leu Val

<210> 75

<211> 34

<212> PRT

<213> *Rickettsia prowazekii*

<400> 75

Asp Arg Phe Tyr Phe Glu Ile Met Arg His Asp Leu Pro Glu Glu Gln
1 - - - 5 - - - 10 - - - 15

Phe Ile Glu Asn Ser Tyr Ile Gln Ile Ala Ser Glu Leu Ser Ile Pro
20 25 30

Ile Val

<210> 76

<211> 34

<212> PRT

<213> *Helicobacter pylori*

<400> 76

Asp Asp Phe Tyr Leu Glu Ile Met Arg His Gly Ile Leu Asp Gln Arg
1 5 10 15

Phe Ile Asp Glu Gln Val Ile Lys Met Ser Leu Glu Thr Gly Leu Lys
20 25 30

Ile Ile

<210> 77

<211> 34

<212> PRT

<213> *Synechocystis* sp.

<400> 77

Asp Asp Tyr Tyr Leu Glu Ile Gln Asp His Gly Ser Val Glu Asp Arg
1 5 10 15

Leu Val Asn Ile Asn Leu Val Lys Ile Ala Gln Glu Leu Asp Ile Lys
20 25 30

Ile Val

<210> 78

<211> 34

<212> PRT

<213> *Mycobacterium tuberculosis*

<400> 78

Asp Asn Tyr Phe Leu Glu Leu Met Asp His Gly Leu Thr Ile Glu Arg
1 5 10 15

Arg Val Arg Asp Gly Leu Leu Glu Ile Gly Arg Ala Leu Asn Ile Pro
20 25 30

Pro Leu

<210> 79

<211> 46

<212> PRT

<213> Escherichia coli

<400> 79

Asn Lys Arg Arg Ala Lys Asn Gly Glu Pro Pro Leu Asp Ile Ala Ala
1 5 10 15

Ile Pro Leu Asp Asp Lys Lys Ser Phe Asp Met Leu Gln Arg Ser Glu
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp
35 40 45

<210> 80

<211> 46

<212> PRT

<213> Vibrio cholerae

<400> 80

Asn Pro Arg Leu Lys Lys Ala Gly Lys Pro Pro Val Arg Ile Glu Ala
1 5 10 15

Ile Pro Leu Asp Asp Ala Arg Ser Phe Arg Asn Leu Gln Asp Ala Lys
20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Glu
35 40 45

<210> 81

<211> 46

<212> PRT

<213> Haemophilus influenzae

<400> 81

Asn Val Arg Met Val Arg Glu Gly Lys Pro Arg Val Asp Ile Ala Ala

1 5 10 15

Ile Pro Leu Asp Asp Pro Glu Ser Phe Glu Leu Leu Lys Arg Ser Glu

20 25 30

Thr Thr Ala Val Phe Gln Leu Glu Ser Arg Gly Met Lys Asp

35 40 45

<210> 82

<211> 46

<212> PRT

<213> Rickettsia prowazekii

<400> 82

Cys Lys Lys Leu Leu Lys Glu Gln Gly Ile Lys Ile Asp Phe Asp Asp

1 5 10 15

Met Thr Phe Asp Asp Lys Lys Thr Tyr Gln Met Leu Cys Lys Gly Lys

20 25 30

Gly Val Gly Val Phe Gln Phe Glu Ser Ile Gly Met Lys Asp

35 40 45

<210> 83

<211> 45

<212> PRT

<213> Helicobacter pylori

<400> 83

Leu Lys Ile Ile Lys Thr Gln His Lys Ile Ser Val Asp Phe Leu Ser

1 5 10 15

Leu Asp Met Asp Asp Pro Lys Val Tyr Lys Thr Ile Gln Ser Gly Asp

20 25 30

Thr Val Gly Ile Phe Gln Ile Glu Ser Gly Met Phe Gln

35 40 45

<210> 84

<211> 46

<212> PRT

<213> Synechocystis sp.

<400> 84

Gln Glu Arg Lys Ala Leu Gln Ile Arg Ala Arg Thr Gly Ser Lys Lys
1 5 10 15

Leu Pro Asp Asp Val Lys Lys Thr His Lys Leu Leu Glu Ala Gly Asp
20 25 30

Leu Glu Gly Ile Phe Gln Leu Glu Ser Gln Gly Met Lys Gln
35 40 45

<210> 85

<211> 46

<212> PRT

<213> Mycobacterium tuberculosis

<400> 85

Ile Asp Asn Val Arg Ala Asn Arg Gly Ile Asp Leu Asp Leu Glu Ser
1 5 10 15

Val Pro Leu Asp Asp Lys Ala Thr Tyr Glu Leu Leu Gly Arg Gly Asp
20 25 30

Thr Leu Gly Val Phe Gln Leu Asp Gly Gly Pro Met Arg Asp
35 40 45

<210> 86

<211> 3729

<212> DNA

<213> Thermus thermophilus

<400> 86

atgggcccggg agctccgctt cgcccacctc caccagcaca cccagttctc cctcctggac 60
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gccttgGCCa tgaccgacca cggcaacctc ttcggggccg tggagttcta caagaaggcc 180
accgaaatgg gcatcaagcc catcctgggc tacgaggcct acgtggcggc ggaaagccgc 240
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aaggacttca cggggtagca gaacctggtg cgcttgGCGa gccgggctta cctggagggg 360
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gcccgcgccc acgaggtcct cctcgccatc cagtccaaga gcaccctgga cgaccccggg 720
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cgctaccg	accggtacac	cgagggcttc	taccgggagg	tcttccgcct	tttggggaag	1020
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gcttgggaga	ggctcatgaa	gagcctcccc	ccttttgccg	gggtcaagga	gtggacggcg	1140
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gaagtggagg	agccgccttt	ggccgaggcc	gccccctgg	acgagatcac	ccggctccgc	3000
tacgagaagg	aggccctggg	gatctacgtc	tccggccacc	ccatcttgcg	gtacccccgg	3060
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gtcctcgccg	aggtggagcg	ggaggagggg	ggcgtgcggg	tgctggccca	ggccgttttg	3360
acctacgagg	agctggagca	ggcccccg	gccctcgagg	tggaggtgga	ggcctccctc	3420
ctggacgacc	ggggggtggc	ccacctgaaa	agcctcctgg	acgagcacgc	ggggaccctc	3480
cccctgtacg	tccgggtcca	gggcgccttc	ggcgaggccc	tcctcgccct	gagggaggtg	3540
cgggtggggg	aggaggctgt	aggcgccgc	gtggttcggg	gcctacctcc	tgcccgaccg	3600
ggaggtcctt	ctccagggcg	gccaggcggg	ggaggccag	gaggcggtgc	ccttctaggg	3660
ggtgggccgt	gagacctagc	gccatcgttc	tcgccggggg	caaggaggcc	tgggcccgc	3720

cccttttgg

3729

<210> 87

<211> 1245

<212> PRT

<213> *Thermus thermophilus*

<400> 87

Met Gly Arg Glu Leu Arg Phe Ala His Leu His Gln His Thr Gln Phe
1 5 10 15

Ser Leu Leu Asp Gly Ala Pro Lys Leu Ser Asp Leu Leu Lys Trp Val
20 25 30

Glu Glu Thr Thr Pro Glu Asp Pro Ala Leu Ala Met Thr Asp His Gly
35 40 45

Asn Leu Phe Gly Ala Val Glu Phe Tyr Lys Lys Ala Thr Glu Met Gly
50 55 60

Ile Lys Pro Ile Leu Gly Tyr Glu Ala Tyr Val Ala Ala Glu Ser Arg
65 70 75 80

Phe Asp Arg Lys Arg Gly Lys Gly Leu Asp Gly Gly Tyr Phe His Leu
85 90 95

Thr Leu Leu Ala Lys Asp Phe Thr Gly Tyr Gln Asn Leu Val Arg Leu
100 105 110

Ala Ser Arg Ala Tyr Leu Glu Gly Phe Tyr Glu Lys Pro Arg Ile Asp
115 120 125

Arg Glu Ile Leu Arg Glu His Ala Glu Gly Leu Ile Ala Leu Ser Gly
130 135 140

Cys Leu Gly Ala Glu Ile Pro Gln Phe Ile Leu Gln Asp Arg Leu Asp
145 150 155 160

Leu Ala Glu Ala Arg Leu Asn Glu Tyr Leu Ser Ile Phe Lys Asp Arg
165 170 175

Phe Phe Ile Glu Ile Gln Asn His Gly Leu Pro Glu Gln Lys Lys Val
180 185 190

Asn Glu Val Leu Lys Glu Phe Ala Arg Lys Tyr Gly Leu Gly Met Val
195 200 205

Ala Thr Asn Asp Gly His Tyr Val Arg Lys Glu Asp Ala Arg Ala His
 210 215 220

Glu Val Leu Leu Ala Ile Gln Ser Lys Ser Thr Leu Asp Asp Pro Gly - - - -
 225 230 235 240

Ala Leu Ala Leu Pro Cys Glu Glu Phe Tyr Val Lys Thr Pro Glu Glu
 245 250 255

Met Arg Ala Met Phe Pro Glu Glu Glu Val Gly Gly Arg Ser Pro Leu
 260 265 270

Thr Thr Pro Trp Arg Ser Pro His Val Gln Arg Gly Ala Ala Ile Gly
 275 280 285

Thr Arg Trp Ser Thr Arg Ile Pro Arg Phe Pro Leu Pro Glu Gly Arg
 290 295 300

Thr Glu Ala Gln Tyr Leu Met Glu Leu Thr Phe Lys Gly Leu Leu Arg
 305 310 315 320

Arg Tyr Pro Asp Arg Ile Thr Glu Gly Phe Tyr Arg Glu Val Phe Arg
 325 330 335

Leu Ser Gly Lys Leu Pro Pro His Gly Asp Gly Glu Ala Leu Ala Glu
 340 345 350

Ala Leu Ala Gln Val Glu Arg Glu Ala Trp Glu Arg Leu Met Lys Ser
 355 360 365

Leu Pro Pro Leu Ala Gly Val Lys Glu Trp Thr Ala Glu Ala Ile Phe
 370 375 380

His Arg Ala Leu Tyr Glu Leu Ser Ala Ile Glu Arg Met Gly Phe Pro
 385 390 395 400

Gly Leu Leu Pro His Arg Pro Gly Leu His Gln Leu Gly Pro Glu Lys
 405 410 415

Gly Val Ser Val Gly Pro Gly Arg Gly Gly Ala Ala Gly Ser Leu Val
 420 425 430

Ala Tyr Ala Val Gly Ile Thr Asn Ile Asp Pro Leu Arg Phe Gly Leu
 435 440 445

Leu Phe Glu Arg Phe Leu Asn Pro Glu Arg Val Ser Met Pro Asp Ile
 450 455 460

Asp Thr Asp Phe Ser Asp Arg Glu Arg Asp Arg Val Ile Gln Tyr Val
 465 470 475 480

Arg Glu Arg Tyr Gly Glu Asp Lys Val Ala Gln Ile Gly Thr Leu Gly
 485 490 495

Ser Leu Ala Ser Lys Ala Ala Leu Lys Glu Val Ala Arg Val Tyr Gly
 500 505 510

Ile Pro Arg Lys Lys Ala Glu Glu Leu Ala Lys Leu Ile Pro Val Gln
 515 520 525

Phe Gly Lys Pro Lys Pro Leu Gln Glu Ala Ile Gln Val Val Pro Glu
 530 535 540

Leu Arg Ala Glu Met Glu Lys Asp Pro Lys Val Arg Glu Val Leu Glu
 545 550 555 560

Val Ala Met Arg Leu Glu Gly Leu Asn Arg His Ala Ser Val His Ala
 565 570 575

Gly Arg Gly Gly Val Phe Ser Glu Pro Leu Thr Asp Leu Val Pro Leu
 580 585 590

Cys Ala Thr Arg Lys Gly Gly Pro Tyr Thr Gln Tyr Asp Met Gly Ala
 595 600 605

Val Glu Ala Leu Gly Leu Leu Lys Met Asp Phe Leu Gly Leu Arg Thr
 610 615 620

Leu Thr Phe Leu Asp Glu Val Lys Arg Ile Val Lys Ala Ser Gln Gly
 625 630 635 640

Val Glu Leu Asp Tyr Asp Ala Leu Pro Leu Asp Asp Pro Lys Thr Phe
 645 650 655

Ala Leu Leu Ser Arg Gly Glu Thr Lys Gly Val Phe Gln Leu Glu Ser
 660 665 670

Gly Gly Met Thr Ala Thr Leu Arg Gly Leu Lys Pro Arg Arg Phe Glu
 675 680 685

Asp Leu Ile Ala Ile Leu Ser Leu Tyr Arg Pro Gly Pro Met Glu His
 690 695 700

Ile Pro Thr Tyr Ile Arg Arg His His Gly Leu Glu Pro Val Ser Tyr
 705 710 715 720

Ser Glu Phe Pro His Ala Glu Lys Tyr Leu Lys Pro Ile Leu Asp Glu
725 730 735

Thr Tyr Gly Ile Pro Val Tyr Gln Glu Gln Ile Met Gln Ile Ala Ser
740 745 750

Ala Val Ala Gly Tyr Ser Leu Gly Glu Ala Asp Leu Leu Arg Arg Ser
755 760 765

Met Gly Lys Lys Lys Val Glu Glu Met Lys Ser His Arg Glu Arg Phe
770 775 780

Val Gln Gly Ala Lys Glu Arg Gly Val Pro Glu Glu Glu Ala Asn Arg
785 790 795 800

Leu Phe Asp Met Leu Glu Ala Phe Ala Asn Tyr Gly Phe Asn Lys Ser
805 810 815

His Ala Ala Ala Tyr Ser Leu Leu Ser Tyr Gln Thr Ala Tyr Val Lys
820 825 830

Ala His Tyr Pro Val Glu Phe Met Ala Ala Leu Leu Ser Val Glu Arg
835 840 845

His Asp Ser Asp Lys Val Ala Glu Tyr Ile Arg Asp Ala Arg Ala Met
850 855 860

Gly Ile Glu Val Leu Pro Pro Asp Val Asn Arg Ser Gly Phe Asp Phe
865 870 875 880

Leu Val Gln Gly Arg Gln Ile Leu Phe Gly Leu Ser Ala Val Lys Asn
885 890 895

Val Gly Glu Ala Ala Ala Glu Ala Ile Leu Arg Glu Arg Glu Arg Gly
900 905 910

Gly Pro Tyr Arg Ser Leu Gly Asp Phe Leu Lys Arg Leu Asp Glu Lys
915 920 925

Val Leu Asn Lys Arg Thr Leu Glu Ser Leu Ile Lys Ala Gly Ala Leu
930 935 940

Asp Gly Phe Gly Glu Arg Ala Arg Leu Leu Ala Ser Leu Glu Gly Leu
945 950 955 960

Leu Lys Trp Ala Ala Glu Asn Arg Glu Lys Ala Arg Ser Gly Met Met
965 970 975

Leu Pro Gly Gly Asn Glu Ala Leu Ala Arg Pro Leu Leu
1235 1240 1245

<210> 88

<211> 198

<212> PRT

<213> *Thermus thermophilus*

<400> 88

Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu Glu
1 5 10 15

Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu Gly
20 25 30

Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly Leu
35 40 45

Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg Arg
50 55 60

Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala Arg
65 70 75 80

Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala Pro
85 90 95

Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp Ala
100 105 110

Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg Pro
115 120 125

Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp Ser
130 135 140

Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly Leu
145 150 155 160

Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His Arg
165 170 175

Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val Tyr
180 185 190

Tyr Met Leu Thr Ser Gly
195

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<210> 89
<211> 182 - - - - -
<212> PRT
<213> Deinococcus radiodurans

<220>
<221> PEPTIDE
<222> (79)
<223> X at position 79 is undefined

<400> 89
Pro Trp Pro Gln Asp Val Val Val Phe Asp Leu Glu Thr Thr Gly Phe
 1             5             10             15

Ser Pro Ala Ser Ala Ala Ile Val Glu Ile Gly Ala Val Arg Ile Val
      20             25             30

Gly Gly Gln Ile Asp Glu Thr Leu Lys Phe Glu Thr Leu Val Arg Pro
      35             40             45

Thr Arg Pro Asp Gly Ser Met Leu Ser Ile Pro Trp Gln Ala Gln Arg
      50             55             60

Val His Gly Ile Ser Asp Glu Met Val Arg Arg Ala Pro Ala Xaa Lys
      65             70             75             80

Asp Val Leu Pro Asp Phe Phe Asp Phe Val Asp Gly Ser Ala Val Val
      85             90             95

Ala His Asn Val Ser Phe Asp Gly Gly Phe Met Arg Ala Gly Ala Glu
      100            105            110

Arg Leu Gly Leu Ser Trp Ala Pro Glu Arg Glu Leu Cys Thr Met Gln
      115            120            125

Leu Ser Arg Arg Ala Phe Pro Arg Glu Arg Thr His Asn Leu Thr Val
      130            135            140

Leu Ala Glu Arg Leu Gly Leu Glu Phe Ala Pro Gly Gly Arg His Arg
      145            150            155            160

Ser Tyr Gly Asp Val Gln Val Thr Ala Gln Ala Tyr Leu Arg Leu Leu
      165            170            175

Glu Leu Leu Gly Glu Arg
      180

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<210> 90
 <211> 201
 <212> PRT
 <213> Bacillus subtilis

<400> 90
 His Gly Ile Lys Met Ile Tyr Gly Met Glu Ala Asn Leu Val Asp Asp
 1 5 10 15
 Gly Val Pro Ile Ala Tyr Asn Ala Ala His Arg Leu Leu Glu Glu Glu
 20 25 30
 Thr Tyr Val Val Phe Asp Val Glu Thr Thr Gly Leu Ser Ala Val Tyr
 35 40 45
 Asp Thr Ile Ile Glu Leu Ala Ala Val Lys Val Lys Gly Gly Glu Ile
 50 55 60
 Ile Asp Lys Phe Glu Ala Phe Ala Asn Pro His Arg Pro Leu Ser Ala
 65 70 75 80
 Thr Ile Ile Glu Leu Thr Gly Ile Thr Asp Asp Met Leu Gln Asp Ala
 85 90 95
 Pro Asp Val Val Asp Val Ile Arg Asp Phe Arg Glu Trp Ile Gly Asp
 100 105 110
 Asp Ile Leu Val Ala His Asn Ala Ser Phe Asp Met Gly Phe Leu Asn
 115 120 125
 Val Ala Tyr Lys Lys Leu Leu Glu Val Glu Lys Ala Lys Asn Pro Val
 130 135 140
 Ile Asp Thr Leu Glu Leu Gly Arg Phe Leu Tyr Pro Glu Phe Lys Asn
 145 150 155 160
 His Arg Leu Asn Thr Leu Cys Lys Lys Phe Asp Ile Glu Leu Thr Gln
 165 170 175
 His His Arg Ala Ile Tyr Asp Thr Glu Ala Thr Ala Tyr Leu Leu Leu
 180 185 190
 Lys Met Leu Lys Asp Ala Ala Glu Lys
 195 200

<210> 91
 <211> 188
 <212> PRT
 <213> Haemophilus influenzae

<220>
 <221> PEPTIDE
 <222> (47)
 <223> X at position 47 is undefined

<220>
 <221> PEPTIDE
 <222> (57)
 <223> X at position 57 is undefined

<400> 91
 Met Ile Asn Pro Asn Arg Gln Ile Val Leu Asp Thr Glu Thr Thr Gly
 1 5 10 15
 Met Asn Gln Leu Gly Ala His Tyr Glu Gly His Cys Ile Ile Glu Ile
 20 25 30
 Gly Ala Val Glu Leu Ile Asn Arg Arg Tyr Thr Gly Asn Asn Xaa His
 35 40 45
 Ile Tyr Ile Lys Pro Asp Arg Pro Xaa Asp Pro Asp Ala Ile Lys Val
 50 55 60
 His Gly Ile Thr Asp Glu Met Leu Ala Asp Lys Pro Glu Phe Lys Glu
 65 70 75 80
 Val Ala Gln Asp Phe Leu Asp Tyr Ile Asn Gly Ala Glu Leu Leu Ile
 85 90 95
 His Asn Ala Pro Phe Asp Val Gly Phe Met Asp Tyr Glu Phe Arg Lys
 100 105 110
 Leu Asn Leu Asn Val Lys Thr Asp Asp Ile Cys Leu Val Thr Asp Thr
 115 120 125
 Leu Gln Met Ala Arg Gln Met Tyr Pro Gly Lys Arg Asn Asn Leu Asp
 130 135 140
 Ala Leu Cys Asp Arg Leu Gly Ile Asp Asn Ser Lys Arg Thr Leu His
 145 150 155 160
 Gly Ala Leu Leu Asp Ala Glu Ile Leu Ala Asp Val Tyr Leu Met Met
 165 170 175

Thr Gly Gly Gln Thr Asn Leu Phe Asp Glu Glu Glu
180 185

<210> 92
<211> 189
<212> PRT
<213> Escherichia coli

<400> 92
Met Ser Thr Ala Ile Thr Arg Gln Ile Val Leu Asp Thr Glu Thr Thr
1 5 10 15
Gly Met Asn Gln Ile Gly Ala His Ser Glu Gly His Lys Ile Ile Glu
20 25 30
Ile Gly Ala Val Glu Val Val Asn Arg Arg Leu Thr Gly Asn Asn Phe
35 40 45
His Val Tyr Leu Lys Asp Arg Leu Val Asp Pro Glu Ala Phe Gly Val
50 55 60
His Gly Ile Ala Val Asp Phe Leu Leu Asp Lys Pro Thr Phe Ala Glu
65 70 75 80
Val Ala Val Glu Phe Met Asp Tyr Ile Arg Gly Ala Glu Leu Val Ile
85 90 95
His Asn Ala Ala Phe Asp Ile Gly Phe Met Asp Tyr Glu Phe Ser Leu
100 105 110
Leu Lys Arg Asp Ile Ala Lys Thr Asn Thr Phe Cys Lys Val Thr Asp
115 120 125
Ser Leu Ala Val Ala Arg Lys Met Phe Pro Gly Lys Arg Asn Ser Leu
130 135 140
Asp Ala Leu Cys Ala Arg Tyr Glu Ile Asp Asn Ser Lys Arg Thr Leu
145 150 155 160
His Gly Ala Leu Leu Asp Ala Gln Ile Leu Ala Glu Val Tyr Leu Ala
165 170 175
Met Thr Gly Gly Gln Thr Ser Met Ala Phe Ala Met Glu
180 185

<210> 93
 <211> 201
 <212> PRT
 <213> Helicobacter pylori.. - - - - -

<400> 93
 Asn Leu Glu Tyr Leu Lys Ala Cys Gly Leu Asn Phe Ile Glu Thr Ser
 1 5 10 15
 Glu Asn Leu Ile Thr Leu Lys Asn Leu Lys Thr Pro Leu Lys Asp Glu
 20 25 30
 Val Phe Ser Phe Ile Asp Leu Glu Thr Thr Gly Ser Cys Pro Ile Lys
 35 40 45
 His Glu Ile Leu Glu Ile Gly Ala Val Gln Val Lys Gly Gly Glu Ile
 50 55 60
 Ile Asn Arg Phe Glu Thr Leu Val Lys Val Lys Ser Val Pro Asp Tyr
 65 70 75 80
 Ile Ala Glu Leu Thr Gly Ile Thr Tyr Glu Asp Thr Leu Asn Ala Pro
 85 90 95
 Ser Ala His Glu Ala Leu Gln Glu Leu Arg Leu Phe Leu Gly Asn Ser
 100 105 110
 Val Phe Val Ala His Asn Ala Asn Phe Asp Tyr Asn Phe Leu Gly Arg
 115 120 125
 Tyr Phe Val Glu Lys Leu His Cys Pro Leu Leu Asn Leu Lys Leu Cys
 130 135 140
 Thr Leu Asp Leu Ser Lys Arg Ala Ile Leu Ser Met Arg Tyr Ser Leu
 145 150 155 160
 Ser Phe Leu Lys Glu Leu Leu Gly Phe Gly Ile Glu Val Ser His Arg
 165 170 175
 Ala Tyr Ala Asp Ala Leu Ala Ser Tyr Lys Leu Phe Glu Ile Cys Leu
 180 185 190
 Leu Asn Leu Pro Ser Tyr Ile Lys Thr
 195 200

<210> 94
 <211> 630

<212> DNA

<213> *Thermus thermophilus*

<400> 94

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atggtggagc ggggtggtgcg gacccttctg gacgggaggt tcctcctgga ggaggggggtg 60
gggctttggg agtggcgcta cccctttccc ctggaggggg aggcggtggt ggtcctggac 120
ctggagacca cggggcttgc cggcctggac gaggtgattg aggtgggcct cctccgcctg 180
gaggggggga ggcgcctccc cttccagagc ctcgcccggc ccctcccgcc cgccgaagcc 240
cgttcgtgga acctcaccgg catcccccgg gaggcctgg aggaggcccc ctccctggag 300
gaggttcttg agaaggccta ccccctccgc ggcgacgcca ccttggtgat ccacaacgcc 360
gcctttgacc tgggcttcct ccgcccggcc ttggagggcc tgggctaccg cctggaaaac 420
cccgtggtgg actccctgcg cttggccaga cggggcttac caggccttag gcgctacggc 480
ctggacgccc tctccgaggt cctggagctt ccccgaagga cctgccaccg ggccctcgag 540
gacgtggagc gcaccctcgc cgtggtgcac gaggtatact atatgcttac gtccggccgt 600
ccccgcacgc tttgggaact cgggaggtag                                     630
```

<210> 95

<211> 210

<212> PRT

<213> *Thermus thermophilus*

<400> 95

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Met Val Glu Arg Val Val Arg Thr Leu Leu Asp Gly Arg Phe Leu Leu
  1             5             10            15

Glu Glu Gly Val Gly Leu Trp Glu Trp Arg Tyr Pro Phe Pro Leu Glu
      20             25            30

Gly Glu Ala Val Val Val Leu Asp Leu Glu Thr Thr Gly Leu Ala Gly
      35             40            45

Leu Asp Glu Val Ile Glu Val Gly Leu Leu Arg Leu Glu Gly Gly Arg
      50             55            60

Arg Leu Pro Phe Gln Ser Leu Val Arg Pro Leu Pro Pro Ala Glu Ala
      65             70            75            80

Arg Ser Trp Asn Leu Thr Gly Ile Pro Arg Glu Ala Leu Glu Glu Ala
      85             90            95

Pro Ser Leu Glu Glu Val Leu Glu Lys Ala Tyr Pro Leu Arg Gly Asp
      100            105            110

Ala Thr Leu Val Ile His Asn Ala Ala Phe Asp Leu Gly Phe Leu Arg
      115            120            125

Pro Ala Leu Glu Gly Leu Gly Tyr Arg Leu Glu Asn Pro Val Val Asp
```

130	135	140
Ser Leu Arg Leu Ala Arg Arg Gly Leu Pro Gly Leu Arg Arg Tyr Gly		
145	150	155 160
Leu Asp Ala Leu Ser Glu Val Leu Glu Leu Pro Arg Arg Thr Cys His		
165	170	175
Arg Ala Leu Glu Asp Val Glu Arg Thr Leu Ala Val Val His Glu Val		
180	185	190
Tyr Tyr Met Leu Thr Ser Gly Arg Pro Arg Thr Leu Trp Glu Leu Gly		
195	200	205
Arg Glx		
210		

<210> 96
 <211> 461
 <212> PRT
 <213> Pseudomonas marcesans

<400> 96

Met Leu Glu Ala Ser Trp Glu Lys Val Gln Ser Ser Leu Lys Gln Asn
1 5 10 15
Leu Ser Lys Pro Ser Tyr Glu Thr Trp Ile Arg Pro Thr Glu Phe Ser
20 25 30
Gly Phe Lys Asn Gly Glu Leu Thr Leu Ile Ala Pro Asn Ser Phe Ser
35 40 45
Ser Ala Trp Leu Lys Asn Asn Tyr Ser Gln Thr Ile Gln Glu Thr Ala
50 55 60
Glu Glu Ile Phe Gly Glu Pro Val Thr Val His Val Lys Val Lys Ala
65 70 75 80
Asn Ala Glu Ser Ser Asp Glu His Tyr Ser Ser Ala Pro Ile Thr Pro
85 90 95
Pro Leu Glu Ala Ser Pro Gly Ser Val Asp Ser Ser Gly Ser Ser Leu
100 105 110
Arg Leu Ser Lys Lys Thr Leu Pro Leu Leu Asn Leu Arg Tyr Val Phe
115 120 125

Ala Ser Arg Arg Arg Pro Val Ser Gln Ala Arg Gln Val Gly Met Tyr
 385 390 395 400

Leu Met Arg Gln Gly Thr Asn Leu Ser Leu Pro Arg Ile Gly Asp Thr -
 405 410 415

Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ala Ile Glu Gln Val
 420 425 430

Glu Lys Lys Leu Ser Ser Asp Pro Gln Ile Ala Ser Gln Val Gln Lys
 435 440 445

Ile Arg Asp Leu Leu Gln Ile Asp Ser Arg Arg Lys Arg
 450 455 460

<210> 97

<211> 447

<212> PRT

<213> Synechocystis sp.

<400> 97

Met Val Ser Cys Glu Asn Leu Trp Gln Gln Ala Leu Ala Ile Leu Ala
 1 5 10 15

Thr Gln Leu Thr Lys Pro Ala Phe Asp Thr Trp Ile Lys Ala Ser Val
 20 25 30

Leu Ile Ser Leu Gly Asp Gly Val Ala Thr Ile Gln Val Glu Asn Gly
 35 40 45

Phe Val Leu Asn His Leu Gln Lys Ser Tyr Gly Pro Leu Leu Met Glu
 50 55 60

Val Leu Thr Asp Leu Thr Gly Gln Glu Ile Thr Val Lys Leu Ile Thr
 65 70 75 80

Asp Gly Leu Glu Pro His Ser Leu Ile Gly Gln Glu Ser Ser Leu Pro
 85 90 95

Met Glu Thr Thr Pro Lys Asn Ala Thr Ala Leu Asn Gly Lys Tyr Thr
 100 105 110

Phe Ser Arg Phe Val Val Gly Pro Thr Asn Arg Met Ala His Ala Ala
 115 120 125

Ser Leu Ala Val Ala Glu Ser Pro Gly Arg Glu Phe Asn Pro Leu Phe
 130 135 140

Leu	Cys	Gly	Gly	Val	Gly	Leu	Gly	Lys	Thr	His	Leu	Met	Gln	Ala	Ile	145	150	155	160
Ala	His	Tyr	Arg	Leu	Glu	Met	Tyr	Pro	Asn	Ala	Lys	Val	Tyr	Tyr	Val	165	170	175	
Ser	Thr	Glu	Arg	Phe	Thr	Asn	Asp	Leu	Ile	Thr	Ala	Ile	Arg	Gln	Asp	180	185	190	
Asn	Met	Glu	Asp	Phe	Arg	Ser	Tyr	Tyr	Arg	Ser	Ala	Asp	Phe	Leu	Leu	195	200	205	
Ile	Asp	Asp	Ile	Gln	Phe	Ile	Lys	Gly	Lys	Glu	Tyr	Thr	Gln	Glu	Glu	210	215	220	
Phe	Phe	His	Thr	Phe	Asn	Ser	Leu	His	Glu	Ala	Gly	Lys	Gln	Val	Val	225	230	235	240
Val	Ala	Ser	Asp	Arg	Ala	Pro	Gln	Arg	Ile	Pro	Gly	Leu	Gln	Asp	Arg	245	250	255	
Leu	Ile	Ser	Arg	Phe	Ser	Met	Gly	Leu	Ile	Ala	Asp	Ile	Gln	Val	Pro	260	265	270	
Asp	Leu	Glu	Thr	Arg	Met	Ala	Ile	Leu	Gln	Lys	Lys	Ala	Glu	Tyr	Asp	275	280	285	
Arg	Ile	Arg	Leu	Pro	Lys	Glu	Val	Ile	Glu	Tyr	Ile	Ala	Ser	His	Tyr	290	295	300	
Thr	Ser	Asn	Ile	Arg	Glu	Leu	Glu	Gly	Ala	Leu	Ile	Arg	Ala	Ile	Ala	305	310	315	320
Tyr	Thr	Ser	Leu	Ser	Asn	Val	Ala	Met	Thr	Val	Glu	Asn	Ile	Ala	Pro	325	330	335	
Val	Leu	Asn	Pro	Pro	Val	Glu	Lys	Val	Ala	Ala	Ala	Pro	Glu	Thr	Ile	340	345	350	
Ile	Thr	Ile	Val	Ala	Gln	His	Tyr	Gln	Leu	Lys	Val	Glu	Glu	Leu	Leu	355	360	365	
Ser	Asn	Ser	Arg	Arg	Arg	Glu	Val	Ser	Leu	Ala	Arg	Gln	Val	Gly	Met	370	375	380	
Tyr	Leu	Met	Arg	Gln	His	Thr	Asp	Leu	Ser	Leu	Pro	Arg	Ile	Gly	Glu	385	390	395	400

Ala Phe Gly Gly Lys Asp His Thr Thr Val Met Tyr Ser Cys Asp Lys
405 410 415

Ile Thr Gln Leu Gln Gln Lys Asp Trp Glu Thr Ser Gln Thr Leu Thr
420 425 430

Ser Leu Ser His Arg Ile Asn Ile Ala Gly Gln Ala Pro Glu Ser
435 440 445

<210> 98

<211> 446

<212> PRT

<213> Bacillus subtilis

<400> 98

Met Glu Asn Ile Leu Asp Leu Trp Asn Gln Ala Leu Ala Gln Ile Glu
1 5 10 15

Lys Lys Leu Ser Lys Pro Ser Phe Glu Thr Trp Met Lys Ser Thr Lys
20 25 30

Ala His Ser Leu Gln Gly Asp Thr Leu Thr Ile Thr Ala Pro Asn Glu
35 40 45

Phe Ala Arg Asp Trp Leu Glu Ser Arg Tyr Leu His Leu Ile Ala Asp
50 55 60

Thr Ile Tyr Glu Leu Thr Gly Glu Glu Leu Ser Ile Lys Phe Val Ile
65 70 75 80

Pro Gln Asn Gln Asp Val Glu Asp Phe Met Pro Lys Pro Gln Val Lys
85 90 95

Lys Ala Val Lys Glu Asp Thr Ser Asp Phe Pro Gln Asn Met Leu Asn
100 105 110

Pro Lys Tyr Thr Phe Asp Thr Phe Val Ile Gly Ser Gly Asn Arg Phe
115 120 125

Ala His Ala Ala Ser Leu Ala Val Ala Glu Ala Pro Ala Lys Ala Tyr
130 135 140

Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr His Leu
145 150 155 160

Met His Ala Ile Gly His Tyr Val Ile Asp His Asn Pro Ser Ala Lys

420

425

430

Gln Leu Gln Gln His Val Lys Glu Ile Lys Glu Gln Leu Lys
 435 _ . 440 _ . 445 _

<210> 99

<211> 507

<212> PRT

<213> Mycobacterium tuberculosis

<400> 99

Met Thr Asp Asp Pro Gly Ser Gly Phe Thr Thr Val Trp Asn Ala Val
 1 5 10 15

Val Ser Glu Leu Asn Gly Asp Pro Lys Val Asp Asp Gly Pro Ser Ser
 20 25 30

Asp Ala Asn Leu Ser Ala Pro Leu Thr Pro Gln Gln Arg Ala Trp Leu
 35 40 45

Asn Leu Val Gln Pro Leu Thr Ile Val Glu Gly Phe Ala Leu Leu Ser
 50 55 60

Val Pro Ser Ser Phe Val Gln Asn Glu Ile Glu Arg His Leu Arg Ala
 65 70 75 80

Pro Ile Thr Asp Ala Leu Ser Arg Arg Leu Gly His Gln Ile Gln Leu
 85 90 95

Gly Val Arg Ile Ala Pro Pro Ala Thr Asp Glu Ala Asp Asp Thr Thr
 100 105 110

Val Pro Pro Ser Glu Asn Pro Ala Thr Thr Ser Pro Asp Thr Thr Thr
 115 120 125

Asp Asn Asp Glu Ile Asp Asp Ser Ala Ala Ala Arg Gly Asp Asn Gln
 130 135 140

His Ser Trp Pro Ser Tyr Phe Thr Glu Arg Pro His Asn Thr Asp Ser
 145 150 155 160

Ala Thr Ala Gly Val Thr Ser Leu Asn Arg Arg Tyr Thr Phe Asp Thr
 165 170 175

Phe Val Ile Gly Ala Ser Asn Arg Phe Ala His Ala Ala Ala Leu Ala
 180 185 190

Tyr Leu Cys Arg Glu Leu Thr Asp Leu Ser Leu Pro Lys Ile Gly Gln
 450 455 460

Ala Phe Gly Arg Asp His Thr Thr Val Met Tyr Ala Gln Arg Lys Ile - - - - -
 465 470 475 480

Leu Ser Glu Met Ala Glu Arg Arg Glu Val Phe Asp His Val Lys Glu
 485 490 495

Leu Thr Thr Arg Ile Arg Gln Arg Ser Lys Arg
 500 505

<210> 100
 <211> 446
 <212> PRT
 <213> Thermus thermophilus

<400> 100
 Met Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
 1 5 10 15

Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
 20 25 30

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
 35 40 45

Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
 50 55 60

Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val
 65 70 75 80

Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro
 85 90 95

Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly
 100 105 110

Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser
 115 120 125

Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu
 130 135 140

Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg
 145 150 155 160

Phe	Pro	His	Met	Arg	Leu	Glu	Tyr	Val	Ser	Thr	Glu	Thr	Phe	Thr	Asn			
				165					170					175				
Glu	Leu	Ile	Asn	Arg	Pro	Ser	Ala	Arg	Asp	Arg	Met	Thr	Glu	Phe	Arg			
			180					185					190					
Glu	Arg	Tyr	Arg	Ser	Val	Asp	Leu	Leu	Leu	Val	Asp	Asp	Val	Gln	Phe			
		195					200					205						
Ile	Ala	Gly	Lys	Glu	Arg	Thr	Gln	Glu	Glu	Phe	Phe	His	Thr	Phe	Asn			
	210					215					220							
Ala	Leu	Tyr	Glu	Ala	His	Lys	Gln	Ile	Ile	Leu	Ser	Ser	Asp	Arg	Pro			
225					230					235					240			
Pro	Lys	Asp	Ile	Leu	Thr	Leu	Glu	Ala	Arg	Leu	Arg	Ser	Arg	Phe	Glu			
			245						250					255				
Trp	Gly	Leu	Ile	Thr	Asp	Asn	Pro	Ala	Pro	Asp	Leu	Glu	Thr	Arg	Ile			
		260						265					270					
Ala	Ile	Leu	Lys	Met	Asn	Ala	Ser	Ser	Gly	Pro	Glu	Asp	Pro	Glu	Asp			
	275						280					285						
Ala	Leu	Glu	Tyr	Ile	Ala	Arg	Gln	Val	Thr	Ser	Asn	Ile	Arg	Glu	Trp			
	290					295					300							
Glu	Gly	Ala	Leu	Met	Arg	Ala	Ser	Pro	Phe	Ala	Ser	Leu	Asn	Gly	Val			
305				310						315				320				
Glu	Leu	Thr	Arg	Ala	Val	Ala	Ala	Lys	Ala	Leu	Arg	His	Leu	Arg	Pro			
			325					330					335					
Arg	Glu	Leu	Glu	Ala	Asp	Pro	Leu	Glu	Ile	Ile	Arg	Lys	Ala	Ala	Gly			
		340						345					350					
Pro	Val	Arg	Pro	Glu	Thr	Pro	Gly	Gly	Ala	His	Gly	Glu	Arg	Arg	Lys			
		355					360					365						
Lys	Glu	Val	Val	Leu	Pro	Arg	Gln	Leu	Ala	Met	Tyr	Leu	Val	Arg	Glu			
	370					375					380							
Leu	Thr	Pro	Ala	Ser	Leu	Pro	Glu	Ile	Gly	Gln	Leu	Phe	Gly	Gly	Arg			
385				390						395					400			
Asp	His	Thr	Thr	Val	Arg	Tyr	Ala	Ile	Gln	Lys	Val	Gln	Glu	Leu	Ala			
				405					410					415				

Gly Lys Pro Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu
 420 425 430

Ala Cys Thr Asp Pro Val Asp Asn Leu Trp Ile Thr Cys Gly
 435 440 445

<210> 101

<211> 467

<212> PRT

<213> Escherichia coli

<400> 101

Met Ser Leu Ser Leu Trp Gln Gln Cys Leu Ala Arg Leu Gln Asp Glu
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Leu Pro Ala Thr Glu Phe Ser Met Trp Ile Arg Pro Leu Gln Ala Glu
 20 25 30

Leu Ser Asp Asn Thr Leu Ala Leu Tyr Ala Pro Asn Arg Phe Val Leu
 35 40 45

Asp Trp Val Arg Asp Lys Tyr Leu Asn Asn Ile Asn Gly Leu Leu Thr
 50 55 60

Ser Phe Cys Gly Ala Asp Ala Pro Gln Leu Arg Phe Glu Val Gly Thr
 65 70 75 80

Lys Pro Val Thr Gln Thr Pro Gln Ala Ala Val Thr Ser Asn Val Ala
 85 90 95

Ala Pro Ala Gln Val Ala Gln Thr Gln Pro Gln Arg Ala Ala Pro Ser
 100 105 110

Thr Arg Ser Gly Trp Asp Asn Val Pro Ala Pro Ala Glu Pro Thr Tyr
 115 120 125

Arg Ser Asn Val Asn Val Lys His Thr Phe Asp Asn Phe Val Glu Gly
 130 135 140

Lys Ser Asn Gln Leu Ala Arg Ala Ala Arg Gln Val Ala Asp Asn
 145 150 155 160

Pro Gly Gly Ala Tyr Asn Pro Leu Phe Leu Tyr Gly Gly Thr Gly Leu
 165 170 175

Gly Lys Thr His Leu Leu His Ala Val Gly Asn Gly Ile Met Ala Arg

435

440

445

Glu Glu Ser His Asp Ile Lys Glu Asp Phe Ser Asn Leu Ile Arg Thr
 450 455 460

Leu Ser Ser
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<210> 102

<211> 440

<212> PRT

<213> *Thermatoga maritima*

<400> 102

Met Lys Glu Arg Ile Leu Gln Glu Ile Lys Thr Arg Val Asn Arg Lys
 1 5 10 15

Ser Trp Glu Leu Trp Phe Ser Ser Phe Asp Val Lys Ser Ile Glu Gly
 20 25 30

Asn Lys Val Val Phe Ser Val Gly Asn Leu Phe Ile Lys Glu Trp Leu
 35 40 45

Glu Lys Lys Tyr Tyr Ser Val Leu Ser Lys Ala Val Lys Val Val Leu
 50 55 60

Gly Asn Asp Ala Thr Phe Glu Ile Thr Tyr Glu Ala Phe Glu Pro His
 65 70 75 80

Ser Ser Tyr Ser Glu Pro Leu Val Lys Lys Arg Ala Val Leu Leu Thr
 85 90 95

Pro Leu Asn Pro Asp Tyr Thr Phe Glu Asn Phe Val Val Gly Pro Gly
 100 105 110

Asn Ser Phe Ala Tyr His Ala Ala Leu Glu Val Ala Lys His Pro Gly
 115 120 125

Arg Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Val Gly Leu Gly Lys Thr
 130 135 140

His Leu Leu Gln Ser Ile Gly Asn Tyr Val Val Gln Asn Glu Pro Asp
 145 150 155 160

Leu Arg Val Met Tyr Ile Thr Ser Glu Lys Phe Leu Asn Asp Leu Val
 165 170 175

— • —

Ile Ser Arg Arg Ala Leu Ser Gly
 435 440

<210> 103
 <211> 457
 <212> PRT
 <213> Helicobacter pylori

<400> 103
 Met Asp Thr Asn Asn Asn Ile Glu Lys Glu Ile Leu Ala Leu Val Lys
 1 5 10 15
 Gln Asn Pro Lys Val Ser Leu Ile Glu Tyr Glu Asn Tyr Phe Ser Gln
 20 25 30
 Leu Lys Tyr Asn Pro Asn Ala Ser Lys Ser Asp Ile Ala Phe Phe Tyr
 35 40 45
 Ala Pro Asn Gln Val Leu Cys Thr Thr Ile Thr Ala Lys Tyr Gly Ala
 50 55 60
 Leu Leu Lys Glu Ile Leu Ser Gln Asn Lys Val Gly Met His Leu Ala
 65 70 75 80
 His Ser Val Asp Val Arg Ile Glu Val Ala Pro Lys Ile Gln Ile Asn
 85 90 95
 Ala Gln Ser Asn Ile Asn Tyr Lys Ala Ile Lys Thr Ser Val Lys Asp
 100 105 110
 Ser Tyr Thr Phe Glu Asn Phe Val Val Gly Ser Cys Asn Asn Thr Val
 115 120 125
 Tyr Glu Ile Ala Lys Lys Val Ala Gln Ser Asp Thr Pro Pro Tyr Asn
 130 135 140
 Pro Val Leu Phe Tyr Gly Gly Thr Gly Leu Gly Lys Thr His Ile Leu
 145 150 155 160
 Asn Ala Ile Gly Asn His Ala Leu Glu Lys His Lys Lys Val Val Leu
 165 170 175
 Val Thr Ser Glu Asp Phe Leu Thr Asp Phe Leu Lys His Leu Asp Asn
 180 185 190
 Lys Thr Met Asp Ser Phe Lys Ala Lys Tyr Arg His Cys Asp Phe Phe
 195 200 205

<210> 104

<211> 1305

<212> DNA

<213> *Thermus thermophilus*

<400> 104

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gagctcgccg tgcccacctc ctttgccctg gactggatcc ggcgccacta cgccggcctc 180
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caaccggaag atacctttaa aacttcgtgg tggggcccaa caactccatg gccccacggc 360
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ggccgtggcc tgggaaagac ctacctgatg cagccgtggg gccactccg tgcgaagcgc 480
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<210> 105

<211> 434

<212> PRT

<213> *Thermus thermophilus*

<400> 105

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Val Ser His Glu Ala Val Trp Gln His Val Leu Glu His Ile Arg Arg
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Ser Ile Thr Glu Val Glu Phe His Thr Trp Phe Glu Arg Ile Arg Pro
          20             25             30

Leu Gly Ile Arg Asp Gly Val Leu Glu Leu Ala Val Pro Thr Ser Phe
      35             40             45

Ala Leu Asp Trp Ile Arg Arg His Tyr Ala Gly Leu Ile Gln Glu Gly
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50	55	60																	
Pro Arg Leu Leu Gly Ala Gln Ala Pro Arg Phe Glu Leu Arg Val Val																			
65		70						75											
Pro Gly Val Val Val Gln Glu Asp Ile Phe Gln Pro Pro Pro Ser Pro																			
		85						90											
Pro Ala Gln Ala Gln Pro Glu Asp Thr Phe Lys Thr Ser Trp Trp Gly																			
		100						105								110			
Pro Thr Thr Pro Trp Pro His Gly Gly Ala Val Ala Val Ala Glu Ser																			
		115						120								125			
Pro Gly Arg Ala Tyr Asn Pro Leu Phe Ile Tyr Gly Gly Arg Gly Leu																			
		130						135								140			
Gly Lys Thr Tyr Leu Met His Ala Val Gly Pro Leu Arg Ala Lys Arg																			
145								150								155			160
Phe Pro His Met Arg Leu Glu Tyr Val Ser Thr Glu Thr Phe Thr Asn																			
								165								170			175
Glu Leu Ile Asn Arg Pro Ser Ala Arg Asp Arg Met Thr Glu Phe Arg																			
								180								185			190
Glu Arg Tyr Arg Ser Val Asp Leu Leu Leu Val Asp Asp Val Gln Phe																			
								195								200			205
Ile Ala Gly Lys Glu Arg Thr Gln Glu Glu Phe Phe His Thr Phe Asn																			
								210								215			220
Ala Leu Tyr Glu Ala His Lys Gln Ile Ile Leu Ser Ser Asp Arg Pro																			
225																230			235
Pro Lys Asp Ile Leu Thr Leu Glu Ala Arg Leu Arg Ser Arg Phe Glu																			
																245			250
Trp Gly Leu Ile Thr Asp Asn Pro Ala Pro Asp Leu Glu Thr Arg Ile																			
																260			265
Ala Ile Leu Lys Met Asn Ala Ser Ser Gly Pro Glu Asp Pro Glu Asp																			
																275			280
Ala Leu Glu Tyr Ile Ala Arg Gln Val Thr Ser Asn Ile Arg Glu Trp																			
																290			295
Glu Gly Ala Leu Met Arg Ala Ser Pro Phe Ala Ser Leu Asn Gly Val																			

305		310		315		320
Glu Leu Thr Arg Ala Val Ala Ala Lys Ala Leu Arg His Leu Arg Pro						
--		325		330		335
Arg Glu Leu Glu Ala Asp Pro Leu Glu Ile Ile Arg Lys Ala Ala Gly						
	340		345		350	
Pro Val Arg Pro Glu Thr Pro Gly Gly Ala His Gly Glu Arg Arg Lys						
	355		360		365	
Lys Glu Val Val Leu Pro Arg Gln Leu Ala Met Tyr Leu Val Arg Glu						
	370		375		380	
Leu Thr Pro Ala Ser Leu Pro Glu Ile Asp Gln Leu Asn Asp Asp Arg						
385		390		395		400
Asp His Thr Thr Val Leu Tyr Ala Ile Gln Lys Val Gln Glu Leu Ala						
	405		410		415	
Glu Ser Asp Arg Glu Val Gln Gly Leu Leu Arg Thr Leu Arg Glu Ala						
	420		425		430	

Cys Thr

<210> 106

<211> 1128

<212> DNA

<213> Thermus thermophilus

<400> 106

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cggatcctcc tctccgccga gggggactac ggcaaggggc aggaggaggt gcccgccag 960
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<210> 107

<211> 376

<212> PRT

<213> *Thermus thermophilus*

<400> 107

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
 1 5 10 15

Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
 20 25 30

Leu Gly Leu Tyr Ala Glu Glu Gly Ala Leu Ile Leu Phe Gly Thr Asn
 35 40 45

Gly Glu Val Asp Leu Glu Val Arg Leu Pro Ala Glu Ala Gln Ser Leu
 50 55 60

Pro Arg Val Leu Val Pro Ala Gln Pro Phe Phe Gln Leu Val Arg Ser
 65 70 75 80

Leu Pro Gly Asp Leu Val Ala Leu Gly Leu Ala Ser Glu Pro Gly Gln
 85 90 95

Gly Gly Gln Leu Glu Leu Ser Ser Gly Arg Phe Arg Thr Arg Leu Ser
 100 105 110

Leu Ala Pro Ala Glu Gly Tyr Pro Glu Leu Leu Val Pro Glu Gly Glu
 115 120 125

Asp Lys Gly Ala Phe Pro Leu Arg Thr Arg Met Pro Ser Gly Glu Leu
 130 135 140

Val Lys Ala Leu Thr His Val Arg Tyr Ala Ala Ser Asn Glu Glu Tyr
 145 150 155 160

Arg Ala Ile Phe Arg Gly Val Gln Leu Glu Phe Ser Pro Gln Gly Phe
 165 170 175

Arg Ala Val Ala Ser Asp Gly Tyr Arg Leu Ala Leu Tyr Asp Leu Pro
 180 185 190

Leu Pro Gln Gly Phe Gln Ala Lys Ala Val Val Pro Ala Arg Ser Val
 195 200 205

Asp Glu Met Val Arg Val Leu Lys Gly Ala Asp Gly Ala Glu Ala Val
 210 215 220

Leu Ala Leu Gly Glu Gly Val Leu Ala Leu Ala Leu Glu Gly Gly Ser
 225 230 235 240

Gly Val Arg Met Ala Leu Arg Leu Met Glu Gly Glu Phe Pro Asp Tyr
 245 250 255

Gln Arg Val Ile Pro Gln Glu Phe Ala Leu Lys Val Gln Val Glu Gly
 260 265 270

Glu Ala Leu Arg Glu Ala Val Arg Arg Val Ser Val Leu Ser Asp Arg
 275 280 285

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
 290 295 300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
 305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
 325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
 340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
 355 360 365

Val Val Val Pro Leu Arg Val Glx
 370 375

<210> 108

<211> 376

<212> PRT

<213> Thermus thermophilus

<400> 108

Met Asn Ile Thr Val Pro Lys Lys Leu Leu Ser Asp Gln Leu Ser Leu
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Leu Glu Arg Ile Val Pro Ser Arg Ser Ala Asn Pro Leu Tyr Thr Tyr
 20 25 30

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		35					40					45				
Gly	Glu	Val	Asp	Leu	Glu	Val	Arg	Leu	Pro	Ala	Glu	Ala	Gln	Ser	Leu	
	50					55					60					
Pro	Arg	Val	Leu	Val	Pro	Ala	Gln	Pro	Phe	Phe	Gln	Leu	Val	Arg	Ser	
65					70					75					80	
Leu	Pro	Gly	Asp	Leu	Val	Ala	Leu	Gly	Leu	Ala	Ser	Glu	Pro	Gly	Gln	
				85					90					95		
Gly	Gly	Gln	Leu	Glu	Leu	Ser	Ser	Gly	Arg	Phe	Arg	Thr	Arg	Leu	Ser	
			100					105					110			
Leu	Ala	Pro	Ala	Glu	Gly	Tyr	Pro	Glu	Leu	Leu	Val	Pro	Glu	Gly	Glu	
		115					120					125				
Asp	Lys	Gly	Ala	Phe	Pro	Leu	Arg	Thr	Arg	Met	Pro	Ser	Gly	Glu	Leu	
	130					135					140					
Val	Lys	Ala	Leu	Thr	His	Val	Arg	Tyr	Ala	Ala	Ser	Asn	Glu	Glu	Tyr	
145					150					155					160	
Arg	Ala	Ile	Phe	Arg	Gly	Val	Gln	Leu	Glu	Phe	Ser	Pro	Gln	Gly	Phe	
				165					170					175		
Arg	Ala	Val	Ala	Ser	Asp	Gly	Tyr	Arg	Leu	Ala	Leu	Tyr	Asp	Leu	Pro	
		180					185						190			
Leu	Pro	Gln	Gly	Phe	Gln	Ala	Lys	Ala	Val	Val	Pro	Ala	Arg	Ser	Val	
		195					200					205				
Asp	Glu	Met	Val	Arg	Val	Leu	Lys	Gly	Ala	Asp	Gly	Ala	Glu	Ala	Val	
	210					215					220					
Leu	Ala	Leu	Gly	Glu	Gly	Val	Leu	Ala	Leu	Ala	Leu	Glu	Gly	Gly	Ser	
225					230				235						240	
Gly	Val	Arg	Met	Ala	Leu	Arg	Leu	Met	Glu	Gly	Glu	Phe	Pro	Asp	Tyr	
				245					250					255		
Gln	Arg	Val	Ile	Pro	Gln	Glu	Phe	Ala	Leu	Lys	Val	Gln	Val	Glu	Gly	
			260					265						270		
Glu	Ala	Leu	Arg	Glu	Ala	Val	Arg	Arg	Val	Ser	Val	Leu	Ser	Asp	Arg	
		275					280					285				

Gln Asn His Arg Val Asp Leu Leu Leu Glu Glu Gly Arg Ile Leu Leu
 290 295 300

Ser Ala Glu Gly Asp Tyr Gly Lys Gly Gln Glu Glu Val Pro Ala Gln
 305 310 315 320

Val Glu Gly Pro Asp Met Ala Val Ala Tyr Asn Ala Arg Tyr Leu Leu
 325 330 335

Glu Ala Leu Ala Pro Val Gly Asp Arg Ala His Leu Gly Ile Ser Gly
 340 345 350

Pro Thr Ser Pro Ser Leu Ile Trp Gly Asp Gly Glu Gly Tyr Arg Ala
 355 360 365

Val Val Val Pro Leu Arg Val Glx
 370 375

<210> 109

<211> 367

<212> PRT

<213> Escherichia coli

<400> 109

Met Lys Phe Thr Val Glu Arg Glu His Leu Leu Lys Pro Leu Gln Gln
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Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn
 20 25 30

Leu Leu Leu Gln Val Ala Asp Gly Thr Leu Ser Leu Thr Gly Thr Asp
 35 40 45

Leu Glu Met Glu Met Val Ala Arg Val Ala Leu Val Gln Pro His Glu
 50 55 60

Pro Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Cys Arg
 65 70 75 80

Gly Leu Pro Glu Gly Ala Glu Ile Ala Val Gln Leu Glu Gly Glu Arg
 85 90 95

Met Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro
 100 105 110

Ala Ala Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe

115							120							125			
Thr	Leu	Pro	Gln	Ala	Thr	Met	Lys	Arg	Leu	Ile	Glu	Ala	Thr	Gln	Phe		
	130						135					140					
Ser	Met	Ala	His	Gln	Asp	Val	Arg	Tyr	Tyr	Leu	Asn	Gly	Met	Leu	Phe		
145					150					155					160		
Glu	Thr	Glu	Gly	Glu	Glu	Leu	Arg	Thr	Val	Ala	Thr	Asp	Gly	His	Arg		
				165					170					175			
Leu	Ala	Val	Cys	Ser	Met	Pro	Ile	Gly	Gln	Ser	Leu	Pro	Ser	His	Ser		
			180					185					190				
Val	Ile	Val	Pro	Arg	Lys	Gly	Val	Ile	Glu	Leu	Met	Arg	Met	Leu	Asp		
	195						200					205					
Gly	Gly	Asp	Asn	Pro	Leu	Arg	Val	Gln	Ile	Gly	Ser	Asn	Asn	Ile	Arg		
	210					215					220						
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225					230					235					240		
Phe	Pro	Asp	Tyr	Arg	Arg	Val	Leu	Pro	Lys	Asn	Pro	Asp	Lys	His	Leu		
				245					250					255			
Glu	Ala	Gly	Cys	Asp	Leu	Leu	Lys	Gln	Ala	Phe	Ala	Arg	Ala	Ala	Ile		
			260					265					270				
Leu	Ser	Asn	Glu	Lys	Phe	Arg	Gly	Val	Arg	Leu	Tyr	Val	Ser	Glu	Asn		
	275						280					285					
Gln	Leu	Lys	Ile	Thr	Ala	Asn	Asn	Pro	Glu	Gln	Glu	Glu	Ala	Glu	Glu		
	290					295					300						
Ile	Leu	Asp	Val	Thr	Tyr	Ser	Gly	Ala	Glu	Met	Glu	Ile	Gly	Phe	Asn		
305					310					315					320		
Val	Ser	Tyr	Val	Leu	Asp	Val	Leu	Asn	Ala	Leu	Lys	Cys	Glu	Asn	Val		
				325					330					335			
Arg	Met	Met	Leu	Thr	Asp	Ser	Val	Ser	Ser	Val	Gln	Ile	Glu	Asp	Ala		
			340					345					350				
Ala	Ser	Gln	Ser	Ala	Ala	Tyr	Val	Val	Met	Pro	Met	Arg	Leu	Glx			
	355						360					365					

<210> 110

<211> 367

<212> PRT

<213> Proteus mirabilis

<400> 110

Met Lys Phe Ile Ile Glu Arg Glu Gln Leu Leu Lys Pro Leu Gln Gln

1

5

10

15

Val Ser Gly Pro Leu Gly Gly Arg Pro Thr Leu Pro Ile Leu Gly Asn

20

25

30

Leu Leu Leu Lys Val Thr Glu Asn Thr Leu Ser Leu Thr Gly Thr Asp

35

40

45

Leu Glu Met Glu Met Met Ala Arg Val Ser Leu Ser Gln Ser His Glu

50

55

60

Ile Gly Ala Thr Thr Val Pro Ala Arg Lys Phe Phe Asp Ile Trp Arg

65

70

75

80

Gly Leu Pro Glu Gly Ala Glu Ile Ser Val Glu Leu Asp Gly Asp Arg

85

90

95

Leu Leu Val Arg Ser Gly Arg Ser Arg Phe Ser Leu Ser Thr Leu Pro

100

105

110

Ala Ser Asp Phe Pro Asn Leu Asp Asp Trp Gln Ser Glu Val Glu Phe

115

120

125

Thr Leu Pro Gln Ala Thr Leu Lys Arg Leu Ile Glu Ser Thr Gln Phe

130

135

140

Ser Met Ala His Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Phe

145

150

155

160

Glu Thr Glu Asn Thr Glu Leu Arg Thr Val Ala Thr Asp Gly His Arg

165

170

175

Leu Ala Val Cys Ala Met Asp Ile Gly Gln Ser Leu Pro Gly His Ser

180

185

190

Val Ile Val Pro Arg Lys Gly Val Ile Glu Leu Met Arg Leu Leu Asp

195

200

205

Gly Ser Gly Glu Ser Leu Leu Gln Leu Gln Ile Gly Ser Asn Asn Leu

210

215

220

Arg	Ala	His	Val	Gly	Asp	Phe	Ile	Phe	Thr	Ser	Lys	Leu	Val	Asp	Gly	225	230	235	240
Arg	Phe	Pro	Asp	Tyr	Arg	Arg	Val	Leu	Pro	Lys	Asn	Pro	Thr	Lys	Thr	245	250	255	
Val	Ile	Ala	Gly	Cys	Asp	Ile	Leu	Lys	Gln	Ala	Phe	Ser	Arg	Ala	Ala	260	265	270	
Ile	Leu	Ser	Asn	Glu	Lys	Phe	Arg	Gly	Val	Arg	Ile	Asn	Leu	Thr	Asn	275	280	285	
Gly	Gln	Leu	Lys	Ile	Thr	Ala	Asn	Asn	Pro	Glu	Gln	Glu	Glu	Ala	Glu	290	295	300	
Glu	Ile	Val	Asp	Val	Gln	Tyr	Gln	Gly	Glu	Glu	Met	Glu	Ile	Gly	Phe	305	310	315	320
Asn	Val	Ser	Tyr	Leu	Leu	Asp	Val	Leu	Asn	Thr	Leu	Lys	Cys	Glu	Glu	325	330	335	
Val	Lys	Leu	Leu	Leu	Thr	Asp	Ala	Val	Ser	Ser	Val	Gln	Val	Glu	Asn	340	345	350	
Val	Ala	Ser	Ala	Ala	Ala	Ala	Tyr	Val	Val	Met	Pro	Met	Arg	Leu	355	360	365		

<210> 111
 <211> 366
 <212> PRT
 <213> Haemophilus influenzae

Met	Gln	Phe	Ser	Ile	Ser	Arg	Glu	Asn	Leu	Leu	Lys	Pro	Leu	Gln	Gln	1	5	10	15
Val	Cys	Gly	Val	Leu	Ser	Asn	Arg	Pro	Asn	Ile	Pro	Val	Leu	Asn	Asn	20	25	30	
Val	Leu	Leu	Gln	Ile	Glu	Asp	Tyr	Arg	Leu	Thr	Ile	Thr	Gly	Thr	Asp	35	40	45	
Leu	Glu	Val	Glu	Leu	Ser	Ser	Gln	Thr	Gln	Leu	Ser	Ser	Ser	Ser	Glu	50	55	60	
Asn	Gly	Thr	Phe	Thr	Ile	Pro	Ala	Lys	Lys	Phe	Leu	Asp	Ile	Cys	Arg	65	70	75	80

Thr Leu Ser Asp Asp Ser Glu Ile Thr Val Thr Phe Glu Gln Asp Arg
85 90 95

Ala Leu Val Gln Ser Gly Arg Ser Arg Phe Thr Leu Ala Thr Gln Pro
100 105 110

Ala Glu Glu Tyr Pro Asn Leu Thr Asp Trp Gln Ser Glu Val Asp Phe
115 120 125

Glu Leu Pro Gln Asn Thr Leu Arg Arg Leu Ile Glu Ala Thr Gln Phe
130 135 140

Ser Met Ala Asn Gln Asp Ala Arg Tyr Phe Leu Asn Gly Met Lys Phe
145 150 155 160

Glu Thr Glu Gly Asn Leu Leu Arg Thr Val Ala Thr Asp Gly His Arg
165 170 175

Leu Ala Val Cys Thr Ile Ser Leu Glu Gln Glu Leu Gln Asn His Ser
180 185 190

Val Ile Leu Pro Arg Lys Gly Val Leu Glu Leu Val Arg Leu Leu Glu
195 200 205

Thr Asn Asp Glu Pro Ala Arg Leu Gln Ile Gly Thr Asn Asn Leu Arg
210 215 220

Val His Leu Lys Asn Thr Val Phe Thr Ser Lys Leu Ile Asp Gly Arg
225 230 235 240

Phe Pro Asp Tyr Arg Arg Val Leu Pro Arg Asn Ala Thr Lys Ile Val
245 250 255

Glu Gly Asn Trp Glu Met Leu Lys Gln Ala Phe Ala Arg Ala Ser Ile
260 265 270

Leu Ser Asn Glu Arg Ala Arg Ser Val Arg Leu Ser Leu Lys Glu Asn
275 280 285

Gln Leu Lys Ile Thr Ala Ser Asn Thr Glu His Glu Glu Ala Glu Glu
290 295 300

Ile Val Asp Val Asn Tyr Asn Gly Glu Glu Leu Glu Val Gly Phe Asn
305 310 315 320

Val Thr Tyr Ile Leu Asp Val Leu Asn Ala Leu Lys Cys Asn Gln Val
325 330 335

Arg Met Cys Leu Thr Asp Ala Phe Ser Ser Cys Leu Ile Glu Asn Cys
 340 345 350

Glu Asp Ser Ser Cys Glu Tyr Val Ile Met Pro Met Arg Leu
 355 360 365

<210> 112

<211> 367

<212> PRT

<213> Pseudomonas putida

<400> 112

Met His Phe Thr Ile Gln Arg Glu Ala Leu Leu Lys Pro Leu Gln Leu
 1 5 10 15

Val Ala Gly Val Val Glu Arg Arg Gln Thr Leu Pro Val Leu Ser Asn
 20 25 30

Val Leu Leu Val Val Gln Gly Gln Gln Leu Ser Leu Thr Gly Thr Asp
 35 40 45

Leu Glu Val Glu Leu Val Gly Arg Val Gln Leu Glu Glu Pro Ala Glu
 50 55 60

Pro Gly Glu Ile Thr Val Pro Ala Arg Lys Leu Met Asp Ile Cys Lys
 65 70 75 80

Ser Leu Pro Asn Asp Ala Leu Ile Asp Ile Lys Val Asp Glu Gln Lys
 85 90 95

Leu Leu Val Lys Ala Gly Arg Ser Arg Phe Thr Leu Ser Thr Leu Pro
 100 105 110

Ala Asn Asp Phe Pro Thr Val Glu Glu Gly Pro Gly Ser Leu Thr Cys
 115 120 125

Asn Leu Glu Gln Ser Lys Leu Arg Arg Leu Ile Glu Arg Thr Ser Phe
 130 135 140

Ala Met Ala Gln Gln Asp Val Arg Tyr Tyr Leu Asn Gly Met Leu Leu
 145 150 155 160

Glu Val Ser Arg Asn Thr Leu Arg Ala Val Ser Thr Asp Gly His Arg
 165 170 175

Leu Ala Leu Cys Ser Met Ser Ala Pro Ile Glu Gln Glu Asp Arg His

Lys Phe Lys Val Leu Ser Asp Asn Gln Glu Glu Glu Thr Ala Glu Asp
 290 295 300

Leu Phe Glu Ile Asp Tyr Phe Gly Glu Lys Ile Glu Ile Ser Ile Asn
 305 310 315 320

Val Tyr Tyr Leu Leu Asp Val Ile Asn Asn Ile Lys Ser Glu Asn Ile
 325 330 335

Ala Leu Phe Leu Asn Lys Ser Lys Ser Ser Ile Gln Ile Glu Ala Glu
 340 345 350

Asn Asn Ser Ser Asn Ala Tyr Val Val Met Leu Leu Lys Arg
 355 360 365

<210> 114

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 114

gtgtggatcc tcgtccccct catgcgcgac caggaagg

39

<210> 115

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 115

gtgtggatcc gtggtgacct tagccac

27

<210> 116

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 116
ttcgtgtccg aggaccttgt ggtccacaac

30

<210> 117
<211> 3514
<212> DNA
<213> *Aquifex aeolicus*

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ataaagatag acgagctcgt gaaaaaggca aaggagtatg gatacaaagc tgtcggaatg 120
tcagaccacg gaaacctctt cggttcgtat aaattctaca aagccctgaa ggcggaagga 180
attaagccca taatcggcac ggaagcctac ttaccacgg gttcgagggt tgacagaaag 240
actaaaacga gcgaggacaa cataaccgac aagtacaacc accacctcat acttatagca 300
aaggacgaaa aggtctaaag aacttaatga agctctcaac cctcgcttac aaagaagggt 360
tttactacaa acccagaatt gattacgaac tccttgaaaa gtacggggag ggccataatg 420
cccttaccgc atgcctgaaa ggtgttccca cctactacgc ttctataaac gaagtgaaaa 480
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gtaagaagaa agcggattta atggctcaga tgaaagacaa gttcatacag ggagcgggtg 2280

```

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```

<210> 118

<211> 1161

<212> PRT

<213> Aquifex aeolicus

<400> 118

```

Met Ser Lys Asp Phe Val His Leu His Leu His Thr Gln Phe Ser Leu
  1                      5                      10                      15

```

```

Leu Asp Gly Ala Ile Lys Ile Asp Glu Leu Val Lys Lys Ala Lys Glu
      20                      25                      30

```

```

Tyr Gly Tyr Lys Ala Val Gly Met Ser Asp His Gly Asn Leu Phe Gly
      35                      40                      45

```

```

Ser Tyr Lys Phe Tyr Lys Ala Leu Lys Ala Glu Gly Ile Lys Pro Ile
      50                      55                      60

```

```

Ile Gly Met Glu Ala Tyr Phe Thr Thr Gly Ser Arg Phe Asp Arg Lys
      65                      70                      75                      80

```

```

Thr Lys Thr Ser Glu Asp Asn Ile Thr Asp Lys Tyr Asn His His Leu
      85                      90                      95

```

```

Ile Leu Ile Ala Lys Asp Asp Lys Gly Leu Lys Asn Leu Met Lys Leu

```


355	360	365																	
Asn	Asp	Ile	Pro	Val	Gly	Pro	Gly	Arg	Gly	Ser	Ala	Gly	Gly	Ser	Leu				
370						375					380								
Val	Ala	Tyr	Ala	Ile	Gly	Ile	Thr	Asp	Val	Asp	Pro	Ile	Lys	His	Gly				
385					390					395					400				
Phe	Leu	Phe	Glu	Arg	Phe	Leu	Asn	Pro	Glu	Arg	Val	Ser	Met	Pro	Asp				
				405					410					415					
Ile	Asp	Val	Asp	Phe	Cys	Gln	Asp	Asn	Arg	Glu	Lys	Val	Ile	Glu	Tyr				
			420					425					430						
Val	Arg	Asn	Lys	Tyr	Gly	His	Asp	Asn	Val	Ala	Gln	Ile	Ile	Thr	Tyr				
	435						440					445							
Asn	Val	Met	Lys	Ala	Lys	Gln	Thr	Leu	Arg	Asp	Val	Ala	Arg	Ala	Met				
450						455					460								
Gly	Leu	Pro	Tyr	Ser	Thr	Ala	Asp	Lys	Leu	Ala	Lys	Leu	Ile	Pro	Gln				
465					470					475					480				
Gly	Asp	Val	Gln	Gly	Thr	Trp	Leu	Ser	Leu	Glu	Glu	Met	Tyr	Lys	Thr				
			485					490					495						
Pro	Val	Glu	Glu	Leu	Leu	Gln	Lys	Tyr	Gly	Glu	His	Arg	Thr	Asp	Ile				
		500						505					510						
Glu	Asp	Asn	Val	Lys	Lys	Phe	Arg	Gln	Ile	Cys	Glu	Glu	Ser	Pro	Glu				
	515						520					525							
Ile	Lys	Gln	Leu	Val	Glu	Thr	Ala	Leu	Lys	Leu	Glu	Gly	Leu	Thr	Arg				
530					535					540									
His	Thr	Ser	Leu	His	Ala	Ala	Gly	Val	Val	Ile	Ala	Pro	Lys	Pro	Leu				
545				550						555					560				
Ser	Glu	Leu	Val	Pro	Leu	Tyr	Tyr	Asp	Lys	Glu	Gly	Glu	Val	Ala	Thr				
			565					570						575					
Gln	Tyr	Asp	Met	Val	Gln	Leu	Glu	Glu	Leu	Gly	Leu	Leu	Lys	Met	Asp				
		580					585						590						
Phe	Leu	Gly	Leu	Lys	Thr	Leu	Thr	Glu	Leu	Lys	Leu	Met	Lys	Glu	Leu				
595						600						605							
Ile	Lys	Glu	Arg	His	Gly	Val	Asp	Ile	Asn	Phe	Leu	Glu	Leu	Pro	Leu				

610	615	620																	
Asp	Asp	Pro	Lys	Val	Tyr	Lys	Leu	Leu	Gln	Glu	Gly	Lys	Thr	Thr	Gly				
625					630					635					640				
Val	Phe	Gln	Leu	Glu	Ser	Arg	Gly	Met	Lys	Glu	Leu	Leu	Lys	Lys	Leu				
				645					650					655					
Lys	Pro	Asp	Ser	Phe	Asp	Asp	Ile	Val	Ala	Val	Leu	Ala	Leu	Tyr	Arg				
			660					665						670					
Pro	Gly	Pro	Leu	Lys	Ser	Gly	Leu	Val	Asp	Thr	Tyr	Ile	Lys	Arg	Lys				
		675					680					685							
His	Gly	Lys	Glu	Pro	Val	Glu	Tyr	Pro	Phe	Pro	Glu	Leu	Glu	Pro	Val				
	690						695					700							
Leu	Lys	Glu	Thr	Tyr	Gly	Val	Ile	Val	Tyr	Gln	Glu	Gln	Val	Met	Lys				
705					710					715					720				
Met	Ser	Gln	Ile	Leu	Ser	Gly	Phe	Thr	Pro	Gly	Glu	Ala	Asp	Thr	Leu				
				725					730						735				
Arg	Lys	Ala	Ile	Gly	Lys	Lys	Lys	Ala	Asp	Leu	Met	Ala	Gln	Met	Lys				
				740					745						750				
Asp	Lys	Phe	Ile	Gln	Gly	Ala	Val	Glu	Arg	Gly	Tyr	Pro	Glu	Glu	Lys				
		755					760						765						
Ile	Arg	Lys	Leu	Trp	Glu	Asp	Ile	Glu	Lys	Phe	Ala	Ser	Tyr	Ser	Phe				
	770					775					780								
Asn	Lys	Ser	His	Ser	Val	Ala	Tyr	Gly	Tyr	Ile	Ser	Tyr	Trp	Thr	Ala				
785					790					795					800				
Tyr	Val	Lys	Ala	His	Tyr	Pro	Ala	Glu	Phe	Phe	Ala	Val	Lys	Leu	Thr				
				805					810					815					
Thr	Glu	Lys	Asn	Asp	Asn	Lys	Phe	Leu	Asn	Leu	Ile	Lys	Asp	Ala	Lys				
			820					825					830						
Leu	Phe	Gly	Phe	Glu	Ile	Leu	Pro	Pro	Asp	Ile	Asn	Lys	Ser	Asp	Val				
		835					840					845							
Gly	Phe	Thr	Ile	Glu	Gly	Glu	Asn	Arg	Ile	Arg	Phe	Gly	Leu	Ala	Arg				
	850					855					860								
Ile	Lys	Gly	Val	Gly	Glu	Glu	Thr	Ala	Lys	Ile	Ile	Val	Glu	Ala	Arg				

865		870		875		880
Lys Lys Tyr Lys Gln Phe Lys Gly Leu Ala Asp Phe Ile Asn Lys Thr						
		885		890		895
Lys Asn Arg Lys Ile Asn Lys Lys Val Val Glu Ala Leu Val Lys Ala						
	900		905		910	
Gly Ala Phe Asp Phe Thr Lys Lys Lys Arg Lys Glu Leu Leu Ala Lys						
	915		920		925	
Val Ala Asn Ser Glu Lys Ala Leu Met Ala Thr Gln Asn Ser Leu Phe						
	930		935		940	
Gly Ala Pro Lys Glu Glu Val Glu Glu Leu Asp Pro Leu Lys Leu Glu						
945		950		955		960
Lys Glu Val Leu Gly Phe Tyr Ile Ser Gly His Pro Leu Asp Asn Tyr						
	965		970		975	
Glu Lys Leu Leu Lys Asn Arg Tyr Thr Pro Ile Glu Asp Leu Glu Glu						
	980		985		990	
Trp Asp Lys Glu Ser Glu Ala Val Leu Thr Gly Val Ile Thr Glu Leu						
	995		1000		1005	
Lys Val Lys Lys Thr Lys Asn Gly Asp Tyr Met Ala Val Phe Asn Leu						
1010		1015		1020		
Val Asp Lys Thr Gly Leu Ile Glu Cys Val Val Phe Pro Gly Val Tyr						
1025		1030		1035		1040
Glu Glu Ala Lys Glu Leu Ile Glu Glu Asp Arg Val Val Val Val Lys						
	1045		1050		1055	
Gly Phe Leu Asp Glu Asp Leu Glu Thr Glu Asn Val Lys Phe Val Val						
	1060		1065		1070	
Lys Glu Val Phe Ser Pro Glu Glu Phe Ala Lys Glu Met Arg Asn Thr						
	1075		1080		1085	
Leu Tyr Ile Phe Leu Lys Arg Glu Gln Ala Leu Asn Gly Val Ala Glu						
1090		1095		1100		
Lys Leu Lys Gly Ile Ile Glu Asn Asn Arg Thr Glu Asp Gly Tyr Asn						
1105		1110		1115		1120
Leu Val Leu Thr Val Asp Leu Gly Asp Tyr Phe Val Asp Leu Ala Leu						

1125

1130

1135

Pro Gln Asp Met Lys Leu Lys Ala Asp Arg Lys Val Val Glu Glu Ile
 1140 1145 1150

Glu Lys Leu Gly Val Lys Val Ile Ile
 1155 1160

<210> 119

<211> 2408

<212> DNA

<213> Aquifex aeolicus

<400> 119

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```

<210> 120

<211> 473

<212> PRT

<213> Aquifex aeolicus

<400> 120

```

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```

```

Glu Val Ile Gly Gln Glu Ala Pro Val Arg Ile Leu Lys Asn Ala Ile
      20             25             30

```

```

Lys Asn Asp Arg Val Ala His Ala Tyr Leu Phe Ala Gly Pro Arg Gly
      35             40             45

```

```

Val Gly Lys Thr Thr Ile Ala Arg Ile Leu Ala Lys Ala Leu Asn Cys
      50             55             60

```

```

Lys Asn Pro Ser Lys Gly Glu Pro Cys Gly Glu Cys Glu Asn Cys Arg
      65             70             75             80

```

```

Glu Ile Asp Arg Gly Val Phe Pro Asp Leu Ile Glu Met Asp Ala Ala
      85             90             95

```

```

Ser Asn Arg Gly Ile Asp Asp Val Arg Ala Leu Lys Glu Ala Val Asn
     100             105             110

```

```

Tyr Lys Pro Ile Lys Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Ala
     115             120             125

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His Met Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu
     130             135             140

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Glu Pro Pro Pro Arg Thr Val Phe Val Leu Cys Thr Thr Glu Tyr Asp
     145             150             155             160

```

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Lys Ile Leu Pro Thr Ile Leu Ser Arg Cys Gln Arg Ile Ile Phe Ser
     165             170             175

```

Lys Val Arg Lys Glu Lys Val Ile Glu Tyr Leu Lys Lys Ile Cys Glu
180 185 190

Lys Glu Gly Ile Glu Cys Glu Glu Gly Ala Leu Glu Val Leu Ala His
195 200 205

Ala Ser Glu Gly Cys Met Arg Asp Ala Ala Ser Leu Leu Asp Gln Ala
210 215 220

Ser Val Tyr Gly Glu Gly Arg Val Thr Lys Glu Val Val Glu Asn Phe
225 230 235 240

Leu Gly Ile Leu Ser Gln Glu Ser Val Arg Ser Phe Leu Lys Leu Leu
245 250 255

Leu Asn Ser Glu Val Asp Glu Ala Ile Lys Phe Leu Arg Glu Leu Ser
260 265 270

Glu Lys Gly Tyr Asn Leu Thr Lys Phe Trp Glu Met Leu Glu Glu Glu
275 280 285

Val Arg Asn Ala Ile Leu Val Lys Ser Leu Lys Asn Pro Glu Ser Val
290 295 300

Val Gln Asn Trp Gln Asp Tyr Glu Asp Phe Lys Asp Tyr Pro Leu Glu
305 310 315 320

Ala Leu Leu Tyr Val Glu Asn Leu Ile Asn Arg Gly Lys Val Glu Ala
325 330 335

Arg Thr Arg Glu Pro Leu Arg Ala Phe Glu Leu Ala Val Ile Lys Ser
340 345 350

Leu Ile Val Lys Asp Ile Ile Pro Val Ser Gln Leu Gly Ser Val Val
355 360 365

Lys Glu Thr Lys Lys Glu Glu Lys Lys Val Glu Val Lys Glu Glu Pro
370 375 380

Lys Val Lys Glu Glu Lys Pro Lys Glu Gln Glu Glu Asp Arg Phe Gln
385 390 395 400

Lys Val Leu Asn Ala Val Asp Gly Lys Ile Leu Lys Arg Ile Leu Glu
405 410 415

Gly Ala Lys Arg Glu Glu Arg Asp Gly Lys Ile Val Leu Lys Ile Glu
420 425 430

Ala Ser Tyr Leu Arg Thr Met Lys Lys Glu Phe Asp Ser Leu Lys Glu
 435 440 445

Thr Phe Pro Phe Leu Glu Phe Glu Pro Val Glu Asp Lys Lys Lys Pro
 450 455 460

Gln Lys Ser Ser Gly Thr Arg Leu Phe
 465 470

<210> 121
 <211> 1090
 <212> DNA
 <213> Aquifex aeolicus

<400> 121
 atgcgcgtta aggtggacag ggaggagctt gaagaggttc ttaaaaaagc aagagaaagc 60
 acggaaaaaa aagccgcaact cccgatactc gcgaacttct tactctccgc aaaagaggaa 120
 aacttaatcg taagggaac ggacttggaa aactaccttg tagtctccgt aaagggggag 180
 gttgaagagg aaggagaggt ttgcgtccac tctcaaaaac tctacgatag agtcaagaac 240
 ttaaattccg cttacgttta ccttcatacg gaaggtgaaa aactcgtcat aacgggagga 300
 aagagtacgt acaaacttcc gacagctccc gcggaggact ttcccgaatt tccagaaatc 360
 gtagaaggag gagaaacact ttccgggaaac cttctcgtta acggaataga aaaggtagag 420
 tacgccatag cgaaggaaga agcgaacata gcccttcagg gaatgtatct gagaggatac 480
 gaggacagaa ttcactttgt gttcggacgg tcacaggctt gcactttatg aacctctacg 540
 taaacattga aaagagtga gacgagtctt ttgcttactt ctccactccc gagtggaaac 600
 tcgccggttag ctcttggaag gagaattccc ggactacatg agtgtcatcc ctgaggagtt 660
 ttccggcgaa gtcttggttg agacagagga agtctttaaag gttttaaaga gggtgaaggc 720
 ttttaagcga ggaaaagttt ttcccgtaga gattacctta agcgaaaacc ttgccatctt 780
 tgagttcgcg gatccggagt tcggagaagc gagagaggaa attgaagtgg agtacacggg 840
 agagcccttt gagataggat tcaacggaaa taccttatgg aggcgcttga cgcctacgac 900
 agcgaagag tgtggttcaa gttcacaacc cccgacacgg ccactttatt ggaggctgaa 960
 gattacgaaa aggaacctta caagtgcata ataatgccga tgagggtgta gccatgaaaa 1020
 aagctttaat ctttttattg agcttgagcc ttttaattcc tgcgttttagc gaagccaaac 1080
 ccaagtcttc 1090

<210> 122
 <211> 363
 <212> PRT
 <213> Aquifex aeolicus

<400> 122
 Met Arg Val Lys Val Asp Arg Glu Glu Leu Glu Glu Val Leu Lys Lys
 1 5 10 15

Ala Arg Glu Ser Thr Glu Lys Lys Ala Ala Leu Pro Ile Leu Ala Asn

275

280

285

Phe Ala Asp Pro Glu Phe Gly Glu Ala Arg Glu Glu Ile Glu Val Glu
 - - - 290 - - - 295 - - - 300 - - -

Tyr Thr Gly Glu Pro Phe Glu Ile Gly Phe Asn Gly Lys Tyr Leu Met
 305 310 315 320

Glu Ala Leu Asp Ala Tyr Asp Ser Glu Arg Val Trp Phe Lys Phe Thr
 325 330 335

Thr Pro Asp Thr Ala Thr Leu Leu Glu Ala Glu Asp Tyr Glu Lys Glu
 340 345 350

Pro Tyr Lys Cys Ile Ile Met Pro Met Arg Val
 355 360

<210> 123

<211> 1093

<212> DNA

<213> Aquifex aeolicus

<400> 123

gtggaaacca caatattcca gttccagaaa acttttttca caaaacctcc gaaggagagg 60
 gtcttcgtcc ttcattggaga agagcagtat ctcataagaa cctttttgtc taagctgaag 120
 gaaaagtacg gggagaatta caccggttctg tgggggggatg agataagcga ggaggaattc 180
 tacactgccc tttccgagac cagtatatctt ggcgggttcaa aggaaaaagc ggtgggtcatt 240
 tacaacttcg gggatttcct gaagaagctc ggaaggaaga aaaaggaaaa agaaaggctt 300
 ataaaagtcc tcagaaacgt aaagagtaac tacgtattta tagtgtacga tgcgaaactc 360
 cagaaacagg aactttcttc ggaacctctg aaatccgtag cgtctttcgg cggatatagt 420
 gtagcaaaca ggctgagcaa ggagaggata aaacagctcg tccttaagaa gttcaaagaa 480
 aaagggataa acgtagaaaa cgatgccctt gaataccttc tccagctcac gggttacaac 540
 ttgatggagc tcaaacttga gggtgaaaaa ctgatagatt acgcaagtga aaagaaaatt 600
 ttaacactcg atgaggtaaa gagagtagcc ttctcagtct cagaaaacgt aaacgtattt 660
 gagttcgttg atttactcct cttaaaagat tacgaaaagg ctcttaaaagt tttggactcc 720
 ctcatcttct tcggaatata cccctccag attatgaaaa tcctgtcctc ctatgctcta 780
 aaactttaca cctcaagag gcttgaagag aaggagagg acctgaataa ggcgatggaa 840
 agcgtgggaa taaagaacaa ctttctcaag atgaagttca aatcttactt aaaggcaaac 900
 tctaaagagg acttgaagaa cctaatacctc tccctccaga ggatagacgc tttttctaaa 960
 ctttactttc aggacacagt gcagttgctg gggattttctt gacctcaaga ctggagaggg 1020
 aagttgtgaa aaatacttct catggtggat aatctttttt atgaagtttg cggtttgctg 1080
 ttttcccggt tct 1093

<210> 124

<211> 350

<212> PRT

<213> Aquifex aeolicus

<400> 124

Val Glu Thr Thr Ile Phe Gln Phe Gln Lys Thr Phe Phe Thr Lys Pro
1 5 10 15

Pro Lys Glu Arg Val Phe Val Leu His Gly Glu Glu Gln Tyr Leu Ile
20 25 30

Arg Thr Phe Leu Ser Lys Leu Lys Glu Lys Tyr Gly Glu Asn Tyr Thr
35 40 45

Val Leu Trp Gly Asp Glu Ile Ser Glu Glu Glu Phe Tyr Thr Ala Leu
50 55 60

Ser Glu Thr Ser Ile Phe Gly Gly Ser Lys Glu Lys Ala Val Val Ile
65 70 75 80

Tyr Asn Phe Gly Asp Phe Leu Lys Lys Leu Gly Arg Lys Lys Lys Glu
85 90 95

Lys Glu Arg Leu Ile Lys Val Leu Arg Asn Val Lys Ser Asn Tyr Val
100 105 110

Phe Ile Val Tyr Asp Ala Lys Leu Gln Lys Gln Glu Leu Ser Ser Glu
115 120 125

Pro Leu Lys Ser Val Ala Ser Phe Gly Gly Ile Val Val Ala Asn Arg
130 135 140

Leu Ser Lys Glu Arg Ile Lys Gln Leu Val Leu Lys Lys Phe Lys Glu
145 150 155 160

Lys Gly Ile Asn Val Glu Asn Asp Ala Leu Glu Tyr Leu Leu Gln Leu
165 170 175

Thr Gly Tyr Asn Leu Met Glu Leu Lys Leu Glu Val Glu Lys Leu Ile
180 185 190

Asp Tyr Ala Ser Glu Lys Lys Ile Leu Thr Leu Asp Glu Val Lys Arg
195 200 205

Val Ala Phe Ser Val Ser Glu Asn Val Asn Val Phe Glu Phe Val Asp
210 215 220

Leu Leu Leu Leu Lys Asp Tyr Glu Lys Ala Leu Lys Val Leu Asp Ser
225 230 235 240

Leu Ile Ser Phe Gly Ile His Pro Leu Gln Ile Met Lys Ile Leu Ser
245 250 255

Ser Tyr Ala Leu Lys Leu Tyr Thr Leu Lys Arg Leu Glu Glu Lys Gly
260 265 270

Glu Asp Leu Asn Lys Ala Met Glu Ser Val Gly Ile Lys Asn Asn Phe
275 280 285

Leu Lys Met Lys Phe Lys Ser Tyr Leu Lys Ala Asn Ser Lys Glu Asp
290 295 300

Leu Lys Asn Leu Ile Leu Ser Leu Gln Arg Ile Asp Ala Phe Ser Lys
305 310 315 320

Leu Tyr Phe Gln Asp Thr Val Gln Leu Leu Arg Asp Phe Leu Thr Ser
325 330 335

Arg Leu Glu Arg Glu Val Val Lys Asn Thr Ser His Gly Gly
340 345 350

<210> 125
<211> 1051
<212> DNA
<213> Aquifex aeolicus

<400> 125
atggaaaaag ttttttttggg aaaactccag aaaaccttgc acataccgag aggactcctt 60
ttttacggca aagaaggaag cggaaagacg aaaacagctt ttgaatttgc aaaaggtatt 120
ttatgtaagg aaaacgtacc tggggatgcg gaagttgtcc ctcttgcaaa cacgtaaagc 180
agctggagga agccttcttt aaaggagaaa tagaagactt taaagtttat aagacaagga 240
cggtaaaaaag cacttcgttt accttatggg cgaacatccc gactttgtgg taataatccc 300
gagcggacat tacataaaga tagaacagat aagggaagtt aagaactttg cctatgtgaa 360
gcccgcacta agcaggagaa aagtaattat aatagacgac gccacgcga tgacctctca 420
ggcggcaaac gctcttttaa aggtatttga agagccacct gcggacacca cctttatctt 480
gaccacgaac aggcgttctg caatcctgcc gactatcctc tccagaactt ttcaagtgga 540
gttcaagggc ttttcagtaa aagaggttat ggaaatagcg aaagtagacg aggaaatagc 600
gaaactctct ggaggcagtc taaaaagggc tatcttacta aaggaaaaca agatatcct 660
aaacaaagta aaggaattct tggaaaacga gccgttaaaa gtttacaagc ttgcaagtga 720
attcgaaaag tgggaacctg aaaagcaaaa actcttcctt gaaattatgg aagaattggt 780
atctcaaaaa ttgaccgaag agaaaaaaga caattacacc taccttcttg atacgatcag 840
actctttaaa gacggactcg caaggggtgt aaacgaacct ctgtggctgt ttacgttagc 900
cgttcaggcg gattaataaa ccgttattga ttccgtaaca tttaaacctt aatctaaatt 960
atgagagcct ttgaaggagg tctggtatgg aaaatttgaa gattagatat atagatacga 1020
ggaagatagg aaccgtgagc ggtgtaaaaag t 1051

<210> 126
 <211> 305
 <212> PRT
 <213> Aquifex_aeolicus

<400> 126
 Met Glu Lys Val Phe Leu Glu Lys Leu Gln Lys Thr Leu His Ile Pro
 1 5 10 15
 Gly Gly Leu Leu Phe Tyr Gly Lys Glu Gly Ser Gly Lys Thr Lys Thr
 20 25 30
 Ala Phe Glu Phe Ala Lys Gly Ile Leu Cys Lys Glu Asn Val Pro Trp
 35 40 45
 Gly Cys Gly Ser Cys Pro Ser Cys Lys His Val Asn Glu Leu Glu Glu
 50 55 60
 Ala Phe Phe Lys Gly Glu Ile Glu Asp Phe Lys Val Tyr Lys Asp Lys
 65 70 75 80
 Asp Gly Lys Lys His Phe Val Tyr Leu Met Gly Glu His Pro Asp Phe
 85 90 95
 Val Val Ile Ile Pro Ser Gly His Tyr Ile Lys Ile Glu Gln Ile Arg
 100 105 110
 Glu Val Lys Asn Phe Ala Tyr Val Lys Pro Ala Leu Ser Arg Arg Lys
 115 120 125
 Val Ile Ile Ile Asp Asp Ala His Ala Met Thr Ser Gln Ala Ala Asn
 130 135 140
 Ala Leu Leu Lys Val Leu Glu Glu Pro Pro Ala Asp Thr Thr Phe Ile
 145 150 155 160
 Leu Thr Thr Asn Arg Arg Ser Ala Ile Leu Pro Thr Ile Leu Ser Arg
 165 170 175
 Thr Phe Gln Val Glu Phe Lys Gly Phe Ser Val Lys Glu Val Met Glu
 180 185 190
 Ile Ala Lys Val Asp Glu Glu Ile Ala Lys Leu Ser Gly Gly Ser Leu
 195 200 205
 Lys Arg Ala Ile Leu Leu Lys Glu Asn Lys Asp Ile Leu Asn Lys Val
 210 215 220

Lys Glu Phe Leu Glu Asn Glu Pro Leu Lys Val Tyr Lys Leu Ala Ser
 225 230 235 240

Glu Phe Glu Lys Trp Glu Pro Glu Lys Gln Lys Leu Phe Leu Glu Ile - - - - -
 245 250 255

Met Glu Glu Leu Val Ser Gln Lys Leu Thr Glu Glu Lys Lys Asp Asn
 260 265 270

Tyr Thr Tyr Leu Leu Asp Thr Ile Arg Leu Phe Lys Asp Gly Leu Ala
 275 280 285

Arg Gly Val Asn Glu Pro Leu Trp Leu Phe Thr Leu Ala Val Gln Ala
 290 295 300

Asp
 305

<210> 127
 <211> 630
 <212> DNA
 <213> Aquifex aeolicus

<400> 127
 atgaacttcc tgaaaaagtt ctttttactg agaaaagctc aaaagtctcc ttacttcgaa 60
 gagttctacg aagaaatcga tttgaaccag aaggtgaaag atgcaagggt tgtagttttt 120
 gactgcgaag ccacagaact cgacgtaaag aaggcaaaac tcctttcaat aggtgcggtt 180
 gaggttaaaa acctggaaat agacctctct aaatcttttt acgagatact caaaagtgac 240
 gagataaagg cggcggagat acatggaata accaggaag acgttgaaaa gtacggaaag 300
 gaaccaaagg aagtaatata cgactttctg aagtacataa agggaagcgt tctcgttggc 360
 tactacgtga agtttgacgt ctactcgtt gagaagtact ccataaagta cttccagtat 420
 ccaatcatca actacaagtt agacctgttt agtttcgtga agagagagta ccagagtggc 480
 aggagtcttg acgaccttat gaaggaactc ggtgtagaaa taagggcaag gcacaacgcc 540
 cttgaagatg cctacataac cgctcttctt ttcttaaagt acgtttaccc gaacagggag 600
 tacagactaa aggatctccc gatcttcctt 630

<210> 128
 <211> 210
 <212> PRT
 <213> Aquifex aeolicus

<400> 128
 Met Asn Phe Leu Lys Lys Phe Leu Leu Leu Arg Lys Ala Gln Lys Ser
 1 5 10 15

Pro Tyr Phe Glu Glu Phe Tyr Glu Glu Ile Asp Leu Asn Gln Lys Val

	20		25		30
Lys Asp Ala Arg Phe Val Val Phe Asp Cys Glu Ala Thr Glu Leu Asp					
35		40		45	
Val Lys Lys Ala Lys Leu Leu Ser Ile Gly Ala Val Glu Val Lys Asn					
50		55		60	
Leu Glu Ile Asp Leu Ser Lys Ser Phe Tyr Glu Ile Leu Lys Ser Asp					
65		70		75	80
Glu Ile Lys Ala Ala Glu Ile His Gly Ile Thr Arg Glu Asp Val Glu					
	85		90		95
Lys Tyr Gly Lys Glu Pro Lys Glu Val Ile Tyr Asp Phe Leu Lys Tyr					
	100		105		110
Ile Lys Gly Ser Val Leu Val Gly Tyr Tyr Val Lys Phe Asp Val Ser					
	115		120		125
Leu Val Glu Lys Tyr Ser Ile Lys Tyr Phe Gln Tyr Pro Ile Ile Asn					
	130		135		140
Tyr Lys Leu Asp Leu Phe Ser Phe Val Lys Arg Glu Tyr Gln Ser Gly					
145		150		155	160
Arg Ser Leu Asp Asp Leu Met Lys Glu Leu Gly Val Glu Ile Arg Ala					
	165		170		175
Arg His Asn Ala Leu Glu Asp Ala Tyr Ile Thr Ala Leu Leu Phe Leu					
	180		185		190
Lys Tyr Val Tyr Pro Asn Arg Glu Tyr Arg Leu Lys Asp Leu Pro Ile					
	195		200		205
Phe Leu					
210					

<210> 129

<211> 526

<212> DNA

<213> Aquifex aeolicus

<400> 129

atgctcaata aggtttttat aataggaaga cttacgggtg accccgttat aacttatcta 60
 ccgagcggaa cgcccgtagt agagtttact ctggcttaca acagaaggta taaaaaccag 120
 aacggtgaat ttcaggagga aagtcacttc tttgacgtaa aggcgtacgg aaaaatggct 180

gaagactggg ctacacgctt ctcgaaagga tacctcgtac tcgtagaggg aagactctcc 240
caggaaaagt gggagaaaaga aggaaagaag ttctcaaagg tcaggataat agcggaaaac 300
gtaagattaa taaacaggcc gaaaggtgct gaacttcaag cagaagaaga ggaggaagtt 360
cctccattg aggaggaaat tgaaaaactc ggtaaagagg aagagaagcc ttttaccgat 420
gaagaggacg aaataccttt ttaattttga ggaggttaaa gtatggtagt gagagctcct 480
aagaagaaag tttgtatgta ctgtgaacaa aagagagagc cagatt 526

<210> 130

<211> 147

<212> PRT

<213> Aquifex aeolicus .

<400> 130

Met Leu Asn Lys Val Phe Ile Ile Gly Arg Leu Thr Gly Asp Pro Val
1 5 10 15

Ile Thr Tyr Leu Pro Ser Gly Thr Pro Val Val Glu Phe Thr Leu Ala
20 25 30

Tyr Asn Arg Arg Tyr Lys Asn Gln Asn Gly Glu Phe Gln Glu Glu Ser
35 40 45

His Phe Phe Asp Val Lys Ala Tyr Gly Lys Met Ala Glu Asp Trp Ala
50 55 60

Thr Arg Phe Ser Lys Gly Tyr Leu Val Leu Val Glu Gly Arg Leu Ser
65 70 75 80

Gln Glu Lys Trp Glu Lys Glu Gly Lys Lys Phe Ser Lys Val Arg Ile
85 90 95

Ile Ala Glu Asn Val Arg Leu Ile Asn Arg Pro Lys Gly Ala Glu Leu
100 105 110

Gln Ala Glu Glu Glu Glu Glu Val Pro Pro Ile Glu Glu Glu Ile Glu
115 120 125

Lys Leu Gly Lys Glu Glu Glu Lys Pro Phe Thr Asp Glu Glu Asp Glu
130 135 140

Ile Pro Phe
145

<210> 131

<211> 1472

<212> DNA

<213> Aquifex aeolicus

<400> 131

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atgcaatttg tggataaaact tccctgtgac- gaatccgccg agagggcggt -tcttggcagt 60
atgcttgaag accccgaaaa catacctctg gtacttgaat accttaaaga agaagacttc 120
tgcatagacg agcacaagct acttttcagg gttcttacia acctctggtc cgagtacggc 180
aataagctcg atttcgtatt aataaaggat caccttgaaa agaaaaactt actccagaaa 240
atacctatag actggctcga agaactctac gaggaggcgg tatcccctga cacgcttgag 300
gaagtctgca aaatagtaaa acaacgttcc gcacagaggg cgataattca actcgggtata 360
gaatcattc acaaaggaaa ggaaaacaaa gactttcaca cattaatcga ggaagcccag 420
agcaggatat tttccatagc ggaaagtgtc acatctacgc agttttacca tgtgaaagac 480
gttgcggaag aagttataga actcatattat aaattcaaaa gctctgacag gctagtcacg 540
ggactcccaa gcggtttcac ggaactcgat ctaaagacga cgggattcca ccctggagac 600
ttaataatac tcgccgcaag acccggtatg gggaaaaccg cctttatgct ctccataatc 660
tacaatctcg caaaagacga gggaaaaccg tcagctgtat tttccttgga aatgagcaag 720
gaacagctcg ttatgagact cctctctatg atgtcggagg tcccactttt caagataagg 780
tctggaagta tatcgaatga agatttaaag aagcttgaag caagcgcaat agaactcgca 840
aagtacgaca tatacctcga cgacacaccc gctctcacta caacggattt aaggataagg 900
gcaagaaagc tcagaaagga aaaggaagtt gagttcgtgg cgggtggacta cttgcaactt 960
ctgagaccgc cagtccgaaa gagttcaaga caggaggaag tggcagaggt ttcaagaaac 1020
ttaaaagccc ttgcaaagga acttcacatt cccgttatgg cacttgcgca gctctcccgt 1080
gaggtggaaa agaggagtga taaaagaccc cagcttgagg acctcagaga atccggacag 1140
atagaacagg acgcagacct aatccttttc ctccacagac ccgagtacta caagaaaaag 1200
ccaaatcccg aagagcaggg tatagcggaa gtgataatag ccaagcaaag gcaaggaccc 1260
acggacattg tgaagctcgc atttattaag gagtacacta agtttgcaaa cctagaagcc 1320
cttcctgaac aacctcctga agaagaggaa ctttccgaaa ttattgaaac acaggaggat 1380
gaaggattcg aagatattga cttctgaaaa ttaaggtttt ataattttat cttggctatc 1440
cggggtagct caatcggcag agcgggtggc tg 1472
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<210> 132

<211> 438

<212> PRT

<213> Aquifex aeolicus

<400> 132

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Met Gln Phe Val Asp Lys Leu Pro Cys Asp Glu Ser Ala Glu Arg Ala
  1             5             10            15

Val Leu Gly Ser Met Leu Glu Asp Pro Glu Asn Ile Pro Leu Val Leu
          20             25            30

Glu Tyr Leu Lys Glu Glu Asp Phe Cys Ile Asp Glu His Lys Leu Leu
          35             40            45

Phe Arg Val Leu Thr Asn Leu Trp Ser Glu Tyr Gly Asn Lys Leu Asp
          50             55            60
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Phe Val Leu Ile Lys Asp His Leu Glu Lys Lys Asn Leu Leu Gln Lys
65 70 75 80

Ile Pro Ile Asp Trp Leu Glu Glu Leu Tyr Glu Glu Ala Val Ser Pro
85 90 95

Asp Thr Leu Glu Glu Val Cys Lys Ile Val Lys Gln Arg Ser Ala Gln
100 105 110

Arg Ala Ile Ile Gln Leu Gly Ile Thr Ser Thr Gln Phe Tyr His Val
115 120 125

Lys Asp Val Ala Glu Glu Val Ile Glu Leu Ile Tyr Lys Phe Lys Ser
130 135 140

Ser Asp Arg Leu Val Thr Gly Leu Pro Ser Gly Phe Thr Glu Leu Asp
145 150 155 160

Leu Lys Thr Thr Gly Phe His Pro Gly Asp Leu Ile Ile Leu Ala Ala
165 170 175

Arg Pro Gly Met Gly Lys Thr Ala Phe Met Leu Ser Ile Ile Tyr Asn
180 185 190

Leu Ala Lys Asp Glu Gly Lys Pro Ser Ala Val Phe Ser Leu Glu Met
195 200 205

Ser Lys Glu Gln Leu Val Met Arg Leu Leu Ser Met Met Ser Glu Val
210 215 220

Pro Leu Phe Lys Ile Arg Ser Gly Ser Ile Ser Asn Glu Asp Leu Lys
225 230 235 240

Lys Leu Glu Ala Ser Ala Ile Glu Leu Ala Lys Tyr Asp Ile Tyr Leu
245 250 255

Asp Asp Thr Pro Ala Leu Thr Thr Thr Asp Leu Arg Ile Arg Ala Arg
260 265 270

Lys Leu Arg Lys Glu Lys Glu Val Glu Phe Val Ala Val Asp Tyr Leu
275 280 285

Gln Leu Leu Arg Pro Pro Val Arg Lys Ser Ser Arg Gln Glu Glu Val
290 295 300

Ala Glu Val Ser Arg Asn Leu Lys Ala Leu Ala Lys Glu Leu His Ile
305 310 315 320

Pro Val Met Ala Leu Ala Gln Leu Ser Arg Glu Val Glu Lys Arg Ser
325 330 335

Asp Lys Arg Pro Gln Leu Ala Asp Leu Arg Glu Ser Gly Gln Ile Glu
340 345 350

Gln Asp Ala Asp Leu Ile Leu Phe Leu His Arg Pro Glu Tyr Tyr Lys
355 360 365

Lys Lys Pro Asn Pro Glu Glu Gln Gly Ile Ala Glu Val Ile Ile Ala
370 375 380

Lys Gln Arg Gln Gly Pro Thr Asp Ile Val Lys Leu Ala Phe Ile Lys
385 390 395 400

Glu Tyr Thr Lys Phe Ala Asn Leu Glu Ala Leu Pro Glu Gln Pro Pro
405 410 415

Glu Glu Glu Glu Leu Ser Glu Ile Ile Glu Thr Gln Glu Asp Glu Gly
420 425 430

Phe Glu Asp Ile Asp Phe
435

<210> 133

<211> 1526

<212> DNA

<213> Aquifex aeolicus

<400> 133

atgtcctcgg acatagacga acttagacgg gaaatagata tagtagacgt catttccgaa 60
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gatacaccct ccttttacgt gtctccaagt aaacaaatat tcaagtgttt cggttgcggg 180
gtagggggag acgcgataaa gttcgtttcc ctttacgagg acatctccta ttttgaagcc 240
gcccttgaac tcgcaaaacg ctacggaaaag aaattagacc ttgaaaagat atcaaaagac 300
gaaaaggat acgtggctct tgacagggtt tgtgatttct acagggaaag ccttctcaaa 360
aacagagagg caagtgagta cgtaaagagt aggggaatag accctaaagt agcgagggaag 420
tttgatcttg ggtacgcacc ttccagtga gactcgtaa aagtcttaaa agagaacgat 480
cttttagagg cttaccttga aactaaaaac ctctttctc ctacgaaggg tgtttacagg 540
gatctctttc ttcggcgtgt cgtgatcccg ataaaggatc cgaggggaag agttataggt 600
ttcggtgga gaggatagt agaggacaaa tctcccaagt acataaactc tccagacagc 660
agggtattta aaaaggggga gaacttattc ggtctttacg aggcaaagga gtatataaag 720
gaagaaggat ttgcgatact tgtggaaggg tactttgacc ttttgagact ttttccgag 780
ggaataagga acgttggtgc accctcgggt acagccctga cccaaaatca ggcaaacctc 840
ctttccaagt tcacaaaaaa ggtctacatc ctttacgacg gagatgatgc gggaagaaag 900
gctatgaaaa gtgccattcc cctactctc agtgcaggag tggaagtta tcccgtttac 960
ctccccgaag gatacgatcc cgacgagttt ataaaggaat tcgggaaaga ggaattaaga 1020

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agactgataa acagctcagg ggagctcttt gaaacgctca taaaaaccgc aagggaaaac 1080
ttagaggaga aaacgcgtga gttcagggtat tatctgggct ttatttcgga tggagtaagg 1140
cgctttgctc tggcttcgga gtttcacacc aagtacaaag ttcctatgga aattttatta 1200
atgaaaattg aaaaaaattc tcaagaaaaa gaaattaaac tctcctttaa ggaaaaaatc 1260
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gaagttctcg agtaccaggt ggataacttg gagaaaacttt ttaacaacat ccttagggat 1440
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actttaataa atttttagag ttagga 1526

```

<210> 134

<211> 498

<212> PRT

<213> Aquifex aeolicus

<400> 134

```

Met Ser Ser Asp Ile Asp Glu Leu Arg Arg Glu Ile Asp Ile Val Asp
  1             5             10             15

```

```

Val Ile Ser Glu Tyr Leu Asn Leu Glu Lys Val Gly Ser Asn Tyr Arg
      20             25             30

```

```

Thr Asn Cys Pro Phe His Pro Asp Asp Thr Pro Ser Phe Tyr Val Ser
      35             40             45

```

```

Pro Ser Lys Gln Ile Phe Lys Cys Phe Gly Cys Gly Val Gly Gly Asp
      50             55             60

```

```

Ala Ile Lys Phe Val Ser Leu Tyr Glu Asp Ile Ser Tyr Phe Glu Ala
      65             70             75             80

```

```

Ala Leu Glu Leu Ala Lys Arg Tyr Gly Lys Lys Leu Asp Leu Glu Lys
      85             90             95

```

```

Ile Ser Lys Asp Glu Lys Val Tyr Val Ala Leu Asp Arg Val Cys Asp
      100            105            110

```

```

Phe Tyr Arg Glu Ser Leu Leu Lys Asn Arg Glu Ala Ser Glu Tyr Val
      115            120            125

```

```

Lys Ser Arg Gly Ile Asp Pro Lys Val Ala Arg Lys Phe Asp Leu Gly
      130            135            140

```

```

Tyr Ala Pro Ser Ser Glu Ala Leu Val Lys Val Leu Lys Glu Asn Asp
      145            150            155            160

```

```

Leu Leu Glu Ala Tyr Leu Glu Thr Lys Asn Leu Leu Ser Pro Thr Lys

```


420 425 430
 Asp Leu Glu Val Leu Asn Leu Ser Pro Glu Leu Lys Glu Leu Ala Val
 435 440 445
 Asn Ala Leu Asn Gly Glu Glu His Leu Leu Pro Lys Glu Val Leu Glu
 450 455 460
 Tyr Gln Val Asp Asn Leu Glu Lys Leu Phe Asn Asn Ile Leu Arg Asp
 465 470 475 480
 Leu Gln Lys Ser Gly Lys Lys Arg Lys Lys Arg Gly Leu Lys Asn Val
 485 490 495

Asn Thr

<210> 135
 <211> 705
 <212> DNA
 <213> Aquifex aeolicus

<400> 135
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 atcccaaaga ggtactggaa cgccaactta gacacttacc accccaagaa cgtatcccag 180
 aacagggcac ttttgacgat aaggggtcttc gtccacaact tcaatcccga ggaagggaaa 240
 gggcttacct ttgtaggatc tcctggagtc ggcaaaactc accttgccgt tgcaacatta 300
 aaagcgattt atgagaagaa gggaatcaga ggatacttct tcgatacgaa ggatctaata 360
 ttcagggttaa aacacttaat ggacgagggg aaggatacaa agtttttaaa aactgtctta 420
 aactcaccgg ttttggttct cgacgacctc ggttctgaga ggctcagtga ctggcagagg 480
 gaactcatct cttacataat cacttacagg tataacaacc ttaagagcac gataataacc 540
 acgaattact cactccagag ggaagaagag agtagcgtga ggataagtgc ggatcttgca 600
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 aagggttccg acctcaggaa gtctaaaaag ctatcaaccc catct 705

<210> 136
 <211> 235
 <212> PRT
 <213> Aquifex aeolicus

<400> 136
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 1 5 10 15
 Lys Thr Glu Asp Asn Lys Val Arg Leu Cys Glu Cys Arg Phe Lys Lys

20					25					30					
Arg	Asp	Val	Asn	Arg	Glu	Leu	Asn	Ile	Pro	Lys	Arg	Tyr	Trp	Asn	Ala
		35						40				45			
Asn	Leu	Asp	Thr	Tyr	His	Pro	Lys	Asn	Val	Ser	Gln	Asn	Arg	Ala	Leu
	50						55				60				
Leu	Thr	Ile	Arg	Val	Phe	Val	His	Asn	Phe	Asn	Pro	Glu	Glu	Gly	Lys
	65					70				75					80
Gly	Leu	Thr	Phe	Val	Gly	Ser	Pro	Gly	Val	Gly	Lys	Thr	His	Leu	Ala
				85					90					95	
Val	Ala	Thr	Leu	Lys	Ala	Ile	Tyr	Glu	Lys	Lys	Gly	Ile	Arg	Gly	Tyr
			100						105				110		
Phe	Phe	Asp	Thr	Lys	Asp	Leu	Ile	Phe	Arg	Leu	Lys	His	Leu	Met	Asp
		115					120					125			
Glu	Gly	Lys	Asp	Thr	Lys	Phe	Leu	Lys	Thr	Val	Leu	Asn	Ser	Pro	Val
	130					135					140				
Leu	Val	Leu	Asp	Asp	Leu	Gly	Ser	Glu	Arg	Leu	Ser	Asp	Trp	Gln	Arg
145					150					155					160
Glu	Leu	Ile	Ser	Tyr	Ile	Ile	Thr	Tyr	Arg	Tyr	Asn	Asn	Leu	Lys	Ser
				165					170					175	
Thr	Ile	Ile	Thr	Thr	Asn	Tyr	Ser	Leu	Gln	Arg	Glu	Glu	Glu	Ser	Ser
			180						185				190		
Val	Arg	Ile	Ser	Ala	Asp	Leu	Ala	Ser	Arg	Leu	Gly	Glu	Asn	Val	Val
		195					200					205			
Ser	Lys	Ile	Tyr	Glu	Met	Asn	Glu	Leu	Leu	Val	Ile	Lys	Gly	Ser	Asp
	210					215					220				
Leu	Arg	Lys	Ser	Lys	Lys	Leu	Ser	Thr	Pro	Ser					
225					230					235					

<210> 137
 <211> 4101
 <212> DNA
 <213> *Thermatoga maritima*

 <400> 137

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gatgttgttt	tcgaaggaaa	caggctgatt	ctgaaaagtc	ttggagattt	cgcgcgggac	300
aggatcgctt	ccaaactcag	aagcacgaaa	aaacagctcg	atgaactgct	gcctcccgga	360
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caaccagaaa	agagagaaga	accaaagggt	gaagaattga	agatcgagga	tgaaaaccac	480
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aaaaagacat	cgggtgaagg	caagatcttc	aaaatagaga	agatcgaggg	gaaaagaacg	600
gtccttctga	tttacctgac	agacggagaa	gattctctga	tctgcaaagt	cttcaacgac	660
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cccgcgatag	ccctcacgga	tcatgggaac	gttcaggcca	taccttactt	ctacgacgcg	960
gcgaaagaag	ctggaataaa	gcccattttc	ggtatcgaag	cgtatctggt	gagtgcgctg	1020
gagcccgta	taaggaatct	ctccgacgat	tcgacgtttg	gagatgccac	gttcgtcgtc	1080
ctcgacttgc	agacgacggg	tctcgacccg	cagggtggatg	agatcatcga	gataggagcg	1140
gtgaagatac	aggggtggcca	gatagtggac	gagtaccaca	ctctcataaa	gccttccagg	1200
gagatctcaa	gaaaaagttc	ggagatcacc	ggaatcactc	aagagatgct	ggaaaacaag	1260
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```

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acggaacagt tcacgctttt c 4101

```

<210> 138

<211> 1367

<212> PRT

<213> *Thermatoga maritima*

<400> 138

```

Met Lys Lys Ile Glu Asn Leu Lys Trp Lys Asn Val Ser Phe Lys Ser
  1                      5                      10                      15

```

```

Leu Glu Ile Asp Pro Asp Ala Gly Val Val Leu Val Ser Val Glu Lys
      20                      25                      30

```

```

Phe Ser Glu Glu Ile Glu Asp Leu Val Arg Leu Leu Glu Lys Lys Thr
      35                      40                      45

```

```

Arg Phe Arg Val Ile Val Asn Gly Val Gln Lys Ser Asn Gly Asp Leu
      50                      55                      60

```

```

Arg Gly Lys Ile Leu Ser Leu Leu Asn Gly Asn Val Pro Tyr Ile Lys
      65                      70                      75                      80

```

```

Asp Val Val Phe Glu Gly Asn Arg Leu Ile Leu Lys Val Leu Gly Asp
      85                      90                      95

```

```

Phe Ala Arg Asp Arg Ile Ala Ser Lys Leu Arg Ser Thr Lys Lys Gln

```


355	360	365																	
Asp	Pro	Gln	Val	Asp	Glu	Ile	Ile	Glu	Ile	Gly	Ala	Val	Lys	Ile	Gln				
370						375					380								
Gly	Gly	Gln	Ile	Val	Asp	Glu	Tyr	His	Thr	Leu	Ile	Lys	Pro	Ser	Arg				
385					390					395					400				
Glu	Ile	Ser	Arg	Lys	Ser	Ser	Glu	Ile	Thr	Gly	Ile	Thr	Gln	Glu	Met				
				405					410					415					
Leu	Glu	Asn	Lys	Arg	Ser	Ile	Glu	Glu	Val	Leu	Pro	Glu	Phe	Leu	Gly				
			420					425					430						
Phe	Leu	Glu	Asp	Ser	Ile	Ile	Val	Ala	His	Asn	Ala	Asn	Phe	Asp	Tyr				
		435					440				445								
Arg	Phe	Leu	Arg	Leu	Trp	Ile	Lys	Lys	Val	Met	Gly	Leu	Asp	Trp	Glu				
	450					455					460								
Arg	Pro	Tyr	Ile	Asp	Thr	Leu	Ala	Leu	Ala	Lys	Ser	Leu	Leu	Lys	Leu				
465				470						475					480				
Arg	Ser	Tyr	Ser	Leu	Asp	Ser	Val	Val	Glu	Lys	Leu	Gly	Leu	Gly	Pro				
				485					490					495					
Phe	Arg	His	His	Arg	Ala	Leu	Asp	Asp	Ala	Arg	Val	Thr	Ala	Gln	Val				
			500					505					510						
Phe	Leu	Arg	Phe	Val	Glu	Met	Met	Lys	Lys	Ile	Gly	Ile	Thr	Lys	Leu				
		515					520						525						
Ser	Glu	Met	Glu	Lys	Leu	Lys	Asp	Thr	Ile	Asp	Tyr	Thr	Ala	Leu	Lys				
	530					535					540								
Pro	Phe	His	Cys	Thr	Ile	Leu	Val	Gln	Asn	Lys	Lys	Gly	Leu	Lys	Asn				
545					550					555					560				
Leu	Tyr	Lys	Leu	Val	Ser	Asp	Ser	Tyr	Ile	Lys	Tyr	Phe	Tyr	Gly	Val				
			565						570					575					
Pro	Arg	Ile	Leu	Lys	Ser	Glu	Leu	Ile	Glu	Asn	Arg	Glu	Gly	Leu	Leu				
			580					585					590						
Val	Gly	Ser	Ala	Cys	Ile	Ser	Gly	Glu	Leu	Gly	Arg	Ala	Ala	Leu	Glu				
	595						600					605							
Gly	Ala	Ser	Asp	Ser	Glu	Leu	Glu	Glu	Ile	Ala	Lys	Phe	Tyr	Asp	Tyr				

610		615		620	
Ile Glu Val Met Pro Leu Asp Val Ile Ala Glu Asp Glu Glu Asp Leu					
625		630		635	640
Asp Arg Glu Arg Leu Lys Glu Val Tyr Arg Lys Leu Tyr Arg Ile Ala					
	645		650		655
Lys Lys Leu Asn Lys Phe Val Val Met Thr Gly Asp Val His Phe Leu					
	660		665		670
Asp Pro Glu Asp Ala Arg Gly Arg Ala Ala Leu Leu Ala Pro Gln Gly					
	675		680		685
Asn Arg Asn Phe Glu Asn Gln Pro Ala Leu Tyr Leu Arg Thr Thr Glu					
	690		695		700
Glu Met Leu Glu Lys Ala Ile Glu Ile Phe Glu Asp Glu Glu Ile Ala					
705		710		715	720
Arg Glu Val Val Ile Glu Asn Pro Asn Arg Ile Ala Asp Met Ile Glu					
	725		730		735
Glu Val Gln Pro Leu Glu Lys Lys Leu His Pro Pro Ile Ile Glu Asn					
	740		745		750
Ala Asp Glu Ile Val Arg Asn Leu Thr Met Lys Arg Ala Tyr Glu Ile					
	755		760		765
Tyr Gly Asp Pro Leu Pro Glu Ile Val Gln Lys Arg Val Glu Lys Glu					
	770		775		780
Leu Asn Ala Ile Ile Asn His Gly Tyr Ala Val Leu Tyr Leu Ile Ala					
785		790		795	800
Gln Glu Leu Val Gln Lys Ser Met Ser Asp Gly Tyr Val Val Gly Ser					
	805		810		815
Arg Gly Ser Val Gly Ser Ser Leu Val Ala Asn Leu Leu Gly Ile Thr					
	820		825		830
Glu Val Asn Pro Leu Pro Pro His Tyr Arg Cys Pro Glu Cys Lys Tyr					
	835		840		845
Phe Glu Val Val Glu Asp Asp Arg Tyr Gly Ala Gly Tyr Asp Leu Pro					
850		855		860	
Asn Lys Asn Cys Pro Arg Cys Gly Ala Pro Leu Arg Lys Asp Gly His					

865		870		875		880
Gly Ile Pro Phe Glu Thr Phe Met Gly Phe Glu Gly Asp Lys Val Pro						
		885		890		895
Asp Ile Asp Leu Asn Phe Ser Gly Glu Tyr Gln Glu Arg Ala His Arg						
	900		905		910	
Phe Val Glu Glu Leu Phe Gly Lys Asp His Val Tyr Arg Ala Gly Thr						
	915		920		925	
Ile Asn Thr Ile Ala Glu Arg Ser Ala Val Gly Tyr Val Arg Ser Tyr						
	930		935		940	
Glu Glu Lys Thr Gly Lys Lys Leu Arg Lys Ala Glu Met Glu Arg Leu						
945		950		955		960
Val Ser Met Ile Thr Gly Val Lys Arg Thr Thr Gly Gln His Pro Gly						
	965		970		975	
Gly Leu Met Ile Ile Pro Lys Asp Lys Glu Val Tyr Asp Phe Thr Pro						
	980		985		990	
Ile Gln Tyr Pro Ala Asn Asp Arg Asn Ala Gly Val Phe Thr Thr His						
	995		1000		1005	
Phe Ala Tyr Glu Thr Ile His Asp Asp Leu Val Lys Ile Asp Ala Leu						
	1010		1015		1020	
Gly His Asp Asp Pro Thr Phe Ile Lys Met Leu Lys Asp Leu Thr Gly						
1025		1030		1035		1040
Ile Asp Pro Met Thr Ile Pro Met Asp Asp Pro Asp Thr Leu Ala Ile						
	1045		1050		1055	
Phe Ser Ser Val Lys Pro Leu Gly Val Asp Pro Val Glu Leu Glu Ser						
	1060		1065		1070	
Asp Val Gly Thr Tyr Gly Ile Pro Glu Phe Gly Thr Glu Phe Val Arg						
	1075		1080		1085	
Gly Met Leu Val Glu Thr Arg Pro Lys Ser Phe Ala Glu Leu Val Arg						
	1090		1095		1100	
Ile Ser Gly Leu Ser His Gly Thr Asp Val Trp Leu Asn Asn Ala Arg						
1105		1110		1115		1120
Asp Trp Ile Asn Leu Gly Tyr Ala Lys Leu Ser Glu Val Ile Ser Cys						

1125	1130	1135
Arg Asp Asp Ile Met Asn Phe Leu Ile His Lys Gly Met Glu Pro Ser		
1140	1145	1150
Leu Ala Phe Lys Ile Met Glu Asn Val Arg Lys Gly Lys Gly Ile Thr		
1155	1160	1165
Glu Glu Met Glu Ser Glu Met Arg Arg Leu Lys Val Pro Glu Trp Phe		
1170	1175	1180
Ile Glu Ser Cys Lys Arg Ile Lys Tyr Leu Phe Pro Lys Ala His Ala		
1185	1190	1195 1200
Val Ala Tyr Val Ser Met Ala Phe Arg Ile Ala Tyr Phe Lys Val His		
1205	1210	1215
Tyr Pro Leu Gln Phe Tyr Ala Ala Tyr Phe Thr Ile Lys Gly Asp Gln		
1220	1225	1230
Phe Asp Pro Val Leu Val Leu Arg Gly Lys Glu Ala Ile Lys Arg Arg		
1235	1240	1245
Leu Arg Glu Leu Lys Ala Met Pro Ala Lys Asp Ala Gln Lys Lys Asn		
1250	1255	1260
Glu Val Ser Val Leu Glu Val Ala Leu Glu Met Ile Leu Arg Gly Phe		
1265	1270	1275 1280
Ser Phe Leu Pro Pro Asp Ile Phe Lys Ser Asp Ala Lys Lys Phe Leu		
1285	1290	1295
Ile Glu Gly Asn Ser Leu Arg Ile Pro Phe Asn Lys Leu Pro Gly Leu		
1300	1305	1310
Gly Asp Ser Val Ala Glu Ser Ile Ile Arg Ala Arg Glu Glu Lys Pro		
1315	1320	1325
Phe Thr Ser Val Glu Asp Leu Met Lys Arg Thr Lys Val Asn Lys Asn		
1330	1335	1340
His Ile Glu Leu Met Lys Ser Leu Gly Val Leu Gly Asp Leu Pro Glu		
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Thr Glu Gln Phe Thr Leu Phe		
1365		

<210> 139

<211> 567

<212> DNA

<213> *Thermatoga maritima*

<400> 139

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aagatctaca gaaacaaagc gtttcactct ctcgtgaatc ccagaataag aatccctgcg 180
ctgattcaga aagttcacgg tatcagcaac atggacatcg tggaagcgcc agacatggac 240
acagtttacg atcttttcag ggattacgtg aagggaacgg tgctcgtgtt tcacaacgcc 300
aacttcgacc tcacttttct ggatatgatg gcaaaggaaa cgggaaactt tccaataacg 360
aatccctaca tcgacacact cgatctttca gaagagatct ttggaaggcc tcattctctc 420
aaatggctct ccgaaagact tggaataaaa accacgatac ggcaccgtgc tcttcagat 480
gccctggtga ccgcaagagt ttttgtgaag cttgttgaat ttcttggtga aaacaggggc 540
aacgaattca tacgtggaaa acggggg 567
```

<210> 140

<211> 189

<212> PRT

<213> *Thermatoga maritima*

<400> 140

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Glu Thr Thr Gly Thr Asp Pro Phe Ala Gly Asp Arg Ile Val Glu Ile
      20             25            30

Ala Ala Val Pro Val Phe Lys Gly Lys Ile Tyr Arg Asn Lys Ala Phe
      35             40            45

His Ser Leu Val Asn Pro Arg Ile Arg Ile Pro Ala Leu Ile Gln Lys
      50             55            60

Val His Gly Ile Ser Asn Met Asp Ile Val Glu Ala Pro Asp Met Asp
      65             70            75            80

Thr Val Tyr Asp Leu Phe Arg Asp Tyr Val Lys Gly Thr Val Leu Val
      85             90            95

Phe His Asn Ala Asn Phe Asp Leu Thr Phe Leu Asp Met Met Ala Lys
      100            105           110

Glu Thr Gly Asn Phe Pro Ile Thr Asn Pro Tyr Ile Asp Thr Leu Asp
      115            120           125
```

Leu Ser Glu Glu Ile Phe Gly Arg Pro His Ser Leu Lys Trp Leu Ser
 130 135 140

Glu Arg Leu Gly Ile Lys Thr Thr Ile Arg His Arg Ala Leu Pro Asp
 145 150 155 160

Ala Leu Val Thr Ala Arg Val Phe Val Lys Leu Val Glu Phe Leu Gly
 165 170 175

Glu Asn Arg Val Asn Glu Phe Ile Arg Gly Lys Arg Gly
 180 185

<210> 141

<211> 1434

<212> DNA

<213> *Thermatoga maritima*

<400> 141

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gtggaagttc tttacaggaa gtacaggcca aagacttttt ctgaggttgt caatcaggat 60
catgtgaaga aggcaataat cgggtgctatt cagaagaaca gcgtggccca cggatacata 120
ttcgccggtc cgaggggaac ggggaagact actcttgcca gaattctcgc aaaatccctg 180
aactgtgaga acagaaaggg agttgaaccc tgcaattcct gcagagcctg cagagagata 240
gacgagggaa ccttcatgga cgtgatagag ctgcacgcgg cctccaacag aggaatagac 300
gagatcagaa gaatcagaga cgccgttgga tacaggccga tggaaagtaa atacaaagtc 360
tacataatag acgaagttca catgctcacg aaagaagcct tcaacgcgct cctcaaaaca 420
ctcgaagaac ctcttcccca cgtcgtgttc gtgctggcaa cgacaaacct tgagaagggtt 480
cctcccacga ttatctcgag atgtcagggtt ttcgagttca gaaacattcc cgacgagctc 540
atcgaagaaga ggctccagga agttgcggag gctgaaggaa tagagataga cagggaagct 600
ctgagcttca tcgcaaaaag agcctctgga ggcttgagag acgcgctcac catgctcgag 660
caggtgtgga agttctcgga aggaaagata gatctcgaga cggtagacag ggcgctcggg 720
ttgataccga tacaggttgt tcgcgattac gtgaacgcta tcttttctgg tgatgtgaaa 780
agggctcttc cgttctcga cgacgtctat tacagcggga aggactacga ggtgctcatt 840
caggaagcag tcgaggatct ggtcgaagac ctggaaaggg agagaggggt ttaccagggtt 900
tcagcgaacg atatagttca ggtttcgaga caacttctga atcttctgag agagataaag 960
ttcgccgaag aaaaacgact cgtctgtaaa gtgggttcgg cttacatagc gacgaggttc 1020
tccaccacaa acgttcagga aaacgatgtc agagaaaaaa acgataattc aaatgtacag 1080
cagaaagaag agaagaaaga aacggtgaag gcaaaagaag aaaaacagga agacagcgag 1140
ttcgagaaac gcttcaaaga actcatggaa gaactgaaag aaaagggcga tctctctatc 1200
tttgctcgtc tcagcctctc agaggtgcag ttgacggag aaaaggtgat tatttctttt 1260
gattcatcga aagctatgca ttacgagttg atgaagaaaa aactgcctga gctggaaaac 1320
atcttttcta gaaaactcgg gaaaaaagta gaagttgaac ttcgactgat gggaaaagaa 1380
gaaacaatcg agaaggtttc tcagaagatc ctgagattgt ttgaacagga ggga 1434
```

<210> 142

<211> 478

<212> PRT

<213> *Thermatoga maritima*

<400> 142

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Met. Glu Val Leu Tyr Arg Lys Tyr Arg Pro Lys Thr Phe Ser Glu Val
  1             5             10             15

Val Asn Gln Asp His Val Lys Lys Ala Ile Ile Gly Ala Ile Gln Lys
      20             25             30

Asn Ser Val Ala His Gly Tyr Ile Phe Ala Gly Pro Arg Gly Thr Gly
      35             40             45

Lys Thr Thr Leu Ala Arg Ile Leu Ala Lys Ser Leu Asn Cys Glu Asn
      50             55             60

Arg Lys Gly Val Glu Pro Cys Asn Ser Cys Arg Ala Cys Arg Glu Ile
      65             70             75             80

Asp Glu Gly Thr Phe Met Asp Val Ile Glu Leu Asp Ala Ala Ser Asn
      85             90             95

Arg Gly Ile Asp Glu Ile Arg Arg Ile Arg Asp Ala Val Gly Tyr Arg
      100            105            110

Pro Met Glu Gly Lys Tyr Lys Val Tyr Ile Ile Asp Glu Val His Met
      115            120            125

Leu Thr Lys Glu Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro
      130            135            140

Pro Ser His Val Val Phe Val Leu Ala Thr Thr Asn Leu Glu Lys Val
      145            150            155            160

Pro Pro Thr Ile Ile Ser Arg Cys Gln Val Phe Glu Phe Arg Asn Ile
      165            170            175

Pro Asp Glu Leu Ile Glu Lys Arg Leu Gln Glu Val Ala Glu Ala Glu
      180            185            190

Gly Ile Glu Ile Asp Arg Glu Ala Leu Ser Phe Ile Ala Lys Arg Ala
      195            200            205

Ser Gly Gly Leu Arg Asp Ala Leu Thr Met Leu Glu Gln Val Trp Lys
      210            215            220

Phe Ser Glu Gly Lys Ile Asp Leu Glu Thr Val His Arg Ala Leu Gly
      225            230            235            240
```

Leu	Ile	Pro	Ile	Gln	Val	Val	Arg	Asp	Tyr	Val	Asn	Ala	Ile	Phe	Ser	245	250	255
Gly	Asp	Val	Lys	Arg	Val	Phe	Thr	Val	Leu	Asp	Asp	Val	Tyr	Tyr	Ser	260	265	270
Gly	Lys	Asp	Tyr	Glu	Val	Leu	Ile	Gln	Glu	Ala	Val	Glu	Asp	Leu	Val	275	280	285
Glu	Asp	Leu	Glu	Arg	Glu	Arg	Gly	Val	Tyr	Gln	Val	Ser	Ala	Asn	Asp	290	295	300
Ile	Val	Gln	Val	Ser	Arg	Gln	Leu	Leu	Asn	Leu	Leu	Arg	Glu	Ile	Lys	305	310	315
Phe	Ala	Glu	Glu	Lys	Arg	Leu	Val	Cys	Lys	Val	Gly	Ser	Ala	Tyr	Ile	325	330	335
Ala	Thr	Arg	Phe	Ser	Thr	Thr	Asn	Val	Gln	Glu	Asn	Asp	Val	Arg	Glu	340	345	350
Lys	Asn	Asp	Asn	Ser	Asn	Val	Gln	Gln	Lys	Glu	Glu	Lys	Lys	Glu	Thr	355	360	365
Val	Lys	Ala	Lys	Glu	Glu	Lys	Gln	Glu	Asp	Ser	Glu	Phe	Glu	Lys	Arg	370	375	380
Phe	Lys	Glu	Leu	Met	Glu	Glu	Leu	Lys	Glu	Lys	Gly	Asp	Leu	Ser	Ile	385	390	395
Phe	Val	Ala	Leu	Ser	Leu	Ser	Glu	Val	Gln	Phe	Asp	Gly	Glu	Lys	Val	405	410	415
Ile	Ile	Ser	Phe	Asp	Ser	Ser	Lys	Ala	Met	His	Tyr	Glu	Leu	Met	Lys	420	425	430
Lys	Lys	Leu	Pro	Glu	Leu	Glu	Asn	Ile	Phe	Ser	Arg	Lys	Leu	Gly	Lys	435	440	445
Lys	Val	Glu	Val	Glu	Leu	Arg	Leu	Met	Gly	Lys	Glu	Glu	Thr	Ile	Glu	450	455	460
Lys	Val	Ser	Gln	Lys	Ile	Leu	Arg	Leu	Phe	Glu	Gln	Glu	Gly			465	470	475

<210> 143

<211> 1098

<212> DNA

<213> *Thermatoga maritima*

<400> 143

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atgaaagtaa cgcgcacgac tcttgaattg aaagacaaaa taaccatcgc ctcaaaagcg 60
ctcgcaaaga aatccgtgaa acccattctt gctggatttc ttttcgaagt gaaagatgga 120
aatttctaca tctgcgcgac cgatctcgag accggagtca aagcaaccgt gaatgccgct 180
gaaatctccg gtgaggcacg ttttgtggtt ccaggagatg tcattcagaa gatggtcaag 240
gttctcccag atgagataac ggaactttct ttagaggggg atgctcttgt tataagttct 300
ggaagcaccg ttttcaggat caccaccatg cccgcggacg aatttcaga gataacgcct 360
gccgagtctg gaataacctt cgaagttgac acttcgctcc tcgaggaaat ggttgaaaag 420
gtcatcttcg ccgctgccaa agacgagttc atgcgaaatc tgaatggagt tttctgggaa 480
ctccacaaga atcttctcag gctggttgca agtgatgggt tcagacttgc acttgctgaa 540
gagcagatag aaaacgagga agaggcgagt ttcttgctct ctttgaagag catgaaagaa 600
gttcaaaacg tgctggacaa cacaacggag ccgactataa cggtgaggta cgatggaaga 660
agggtttctc tgtcgacaaa tgatgtagaa acggtgatga gagtggtcga cgctgaattt 720
cccgattaca aaaggtgat ccccgaaact ttcaaaacga aagtgggtgt ttccagaaaa 780
gaactcaggg aatctttgaa gaggtgatg gtgattgcca gcaaggaag cgagtccgtg 840
aagttcgaaa tagaagaaaa cgttatgaga cttgtgagca agagcccgga ttatggagaa 900
gtggtcgatg aagttgaagt tcaaaaagaa ggggaagatc tcgtgatcgc tttcaaccgc 960
aagttcatcg aggacgtttt gaagcacatt gagactgaag aaatcgaaat gaacttcgtt 1020
gattctacca gtccatgtca gataaatcca ctcgatattt ctggatacct ttacatagtg 1080
atgcccatac gactggca                                     1098
```

<210> 144

<211> 366

<212> PRT

<213> *Thermatoga maritima*

<400> 144

```
Met Lys Val Thr Val Thr Thr Leu Glu Leu Lys Asp Lys Ile Thr Ile
  1                      5                      10                      15

Ala Ser Lys Ala Leu Ala Lys Lys Ser Val Lys Pro Ile Leu Ala Gly
    20                      25                      30

Phe Leu Phe Glu Val Lys Asp Gly Asn Phe Tyr Ile Cys Ala Thr Asp
    35                      40                      45

Leu Glu Thr Gly Val Lys Ala Thr Val Asn Ala Ala Glu Ile Ser Gly
    50                      55                      60

Glu Ala Arg Phe Val Val Pro Gly Asp Val Ile Gln Lys Met Val Lys
    65                      70                      75                      80

Val Leu Pro Asp Glu Ile Thr Glu Leu Ser Leu Glu Gly Asp Ala Leu
    85                      90                      95
```

Val	Ile	Ser	Ser	Gly	Ser	Thr	Val	Phe	Arg	Ile	Thr	Thr	Met	Pro	Ala	
			100					105					110			
Asp	Glu	Phe	Pro	Glu	Ile	Thr	Pro	Ala	Glu	Ser	Gly	Ile	Thr	Phe	Glu	
		115					120					125				
Val	Asp	Thr	Ser	Leu	Leu	Glu	Glu	Met	Val	Glu	Lys	Val	Ile	Phe	Ala	
	130					135					140					
Ala	Ala	Lys	Asp	Glu	Phe	Met	Arg	Asn	Leu	Asn	Gly	Val	Phe	Trp	Glu	
145					150					155					160	
Leu	His	Lys	Asn	Leu	Leu	Arg	Leu	Val	Ala	Ser	Asp	Gly	Phe	Arg	Leu	
			165					170						175		
Ala	Leu	Ala	Glu	Glu	Gln	Ile	Glu	Asn	Glu	Glu	Glu	Ala	Ser	Phe	Leu	
			180					185					190			
Leu	Ser	Leu	Lys	Ser	Met	Lys	Glu	Val	Gln	Asn	Val	Leu	Asp	Asn	Thr	
	195						200					205				
Thr	Glu	Pro	Thr	Ile	Thr	Val	Arg	Tyr	Asp	Gly	Arg	Arg	Val	Ser	Leu	
	210					215					220					
Ser	Thr	Asn	Asp	Val	Glu	Thr	Val	Met	Arg	Val	Val	Asp	Ala	Glu	Phe	
225					230					235					240	
Pro	Asp	Tyr	Lys	Arg	Val	Ile	Pro	Glu	Thr	Phe	Lys	Thr	Lys	Val	Val	
			245						250					255		
Val	Ser	Arg	Lys	Glu	Leu	Arg	Glu	Ser	Leu	Lys	Arg	Val	Met	Val	Ile	
			260					265					270			
Ala	Ser	Lys	Gly	Ser	Glu	Ser	Val	Lys	Phe	Glu	Ile	Glu	Glu	Asn	Val	
		275					280					285				
Met	Arg	Leu	Val	Ser	Lys	Ser	Pro	Asp	Tyr	Gly	Glu	Val	Val	Asp	Glu	
	290					295					300					
Val	Glu	Val	Gln	Lys	Glu	Gly	Glu	Asp	Leu	Val	Ile	Ala	Phe	Asn	Pro	
305					310					315					320	
Lys	Phe	Ile	Glu	Asp	Val	Leu	Lys	His	Ile	Glu	Thr	Glu	Glu	Ile	Glu	
			325					330						335		
Met	Asn	Phe	Val	Asp	Ser	Thr	Ser	Pro	Cys	Gln	Ile	Asn	Pro	Leu	Asp	
			340					345					350			

Ile Ser Gly Tyr Leu Tyr Ile Val Met Pro Ile Arg Leu Ala
 355 360 365

<210> 145
 <211> 972
 <212> DNA
 <213> *Thermatoga maritima*

<400> 145
 atgccagtca cgtttctcac aggtactgca gaaactcaga aggaagaatt gataaagaaa 60
 ctctgaagg atggtaacgt ggagtacata aggatccatc cggaggatcc cgacaagatc 120
 gatttcataa ggtctttact caggacaaaag acgatctttt ccaacaagac gatcattgac 180
 atcgtcaatt tcgatgagtg gaaagcacag gagcagaagc gtctcgttga acttttgaaa 240
 aacgtaccgg aagacgttca tatcttcatc cgttctcaaa aaacaggtgg aaagggagta 300
 gcgctggagc ttccgaagcc atgggaaacg gacaagtggc ttgagtggat agaaaagcgc 360
 ttcagggaga atggtttgct catcgataaa gatgcccttc agctgttttt ctccaagggt 420
 ggaacgaacg acctgatcat agaaagggag attgaaaaac tgaaagctta ttccgaggac 480
 agaaagataa cggtagaaga cgtggaagag gtcgttttta cctatcagac tccgggatac 540
 gatgattttt gctttgctgt ttccgaagga aaaaggaagc tcgctcactc tcttctgtcg 600
 cagctgtgga aaaccacaga gtccgtggtg attgccactg tccttgcgaa tcacttcttg 660
 gatctcttca aaatcctcgt tcttgtagaca aagaaaagat actacacctg gcctgatgtg 720
 tccaggtgtg ccaaagagct gggaattccc gttcctcgtg tggctcgttt cctcggtttc 780
 tcctttaaga cctggaaatt caaggtgatg aaccacctcc tctactacga tgtgaagaag 840
 gtagaaaaga tactgagggg tctctacgat ctggacagag ccgtgaaaag cgaagaagat 900
 ccaaaaccgt tcttccacga gttcatagaa gaggtggcac tggatgtata ttctcttcag 960
 agagatgaag aa 972

<210> 146
 <211> 324
 <212> PRT
 <213> *Thermatoga maritima*

<400> 146
 Met Pro Val Thr Phe Leu Thr Gly Thr Ala Glu Thr Gln Lys Glu Glu
 1 5 10 15
 Leu Ile Lys Lys Leu Leu Lys Asp Gly Asn Val Glu Tyr Ile Arg Ile
 20 25 30
 His Pro Glu Asp Pro Asp Lys Ile Asp Phe Ile Arg Ser Leu Leu Arg
 35 40 45
 Thr Lys Thr Ile Phe Ser Asn Lys Thr Ile Ile Asp Ile Val Asn Phe
 50 55 60

Asp	Glu	Trp	Lys	Ala	Gln	Glu	Gln	Lys	Arg	Leu	Val	Glu	Leu	Leu	Lys				
65					70					75					80				
Asn	Val	Pro	Glu	Asp	Val	His	Ile	Phe	Ile	Arg	Ser	Gln	Lys	Thr	Gly				
				85					90					95					
Gly	Lys	Gly	Val	Ala	Leu	Glu	Leu	Pro	Lys	Pro	Trp	Glu	Thr	Asp	Lys				
			100					105					110						
Trp	Leu	Glu	Trp	Ile	Glu	Lys	Arg	Phe	Arg	Glu	Asn	Gly	Leu	Leu	Ile				
			115				120					125							
Asp	Lys	Asp	Ala	Leu	Gln	Leu	Phe	Phe	Ser	Lys	Val	Gly	Thr	Asn	Asp				
	130					135					140								
Leu	Ile	Ile	Glu	Arg	Glu	Ile	Glu	Lys	Leu	Lys	Ala	Tyr	Ser	Glu	Asp				
145					150					155					160				
Arg	Lys	Ile	Thr	Val	Glu	Asp	Val	Glu	Glu	Val	Val	Phe	Thr	Tyr	Gln				
				165					170						175				
Thr	Pro	Gly	Tyr	Asp	Asp	Phe	Cys	Phe	Ala	Val	Ser	Glu	Gly	Lys	Arg				
			180					185						190					
Lys	Leu	Ala	His	Ser	Leu	Leu	Ser	Gln	Leu	Trp	Lys	Thr	Thr	Glu	Ser				
		195					200					205							
Val	Val	Ile	Ala	Thr	Val	Leu	Ala	Asn	His	Phe	Leu	Asp	Leu	Phe	Lys				
		210				215					220								
Ile	Leu	Val	Leu	Val	Thr	Lys	Lys	Arg	Tyr	Tyr	Thr	Trp	Pro	Asp	Val				
225					230					235					240				
Ser	Arg	Val	Ser	Lys	Glu	Leu	Gly	Ile	Pro	Val	Pro	Arg	Val	Ala	Arg				
				245					250					255					
Phe	Leu	Gly	Phe	Ser	Phe	Lys	Thr	Trp	Lys	Phe	Lys	Val	Met	Asn	His				
			260					265					270						
Leu	Leu	Tyr	Tyr	Asp	Val	Lys	Lys	Val	Arg	Lys	Ile	Leu	Arg	Asp	Leu				
		275					280					285							
Tyr	Asp	Leu	Asp	Arg	Ala	Val	Lys	Ser	Glu	Glu	Asp	Pro	Lys	Pro	Phe				
	290					295					300								
Phe	His	Glu	Phe	Ile	Glu	Glu	Val	Ala	Leu	Asp	Val	Tyr	Ser	Leu	Gln				
305					310					315					320				

Arg Asp Glu Glu

<210> 147

<211> 936

<212> DNA

<213> *Thermatoga maritima*

<400> 147

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gaaaagtctg aaggaatatc catcctcata aatggagaag atctctcgta tccgagagaa 120
gtatcccttg aacttcccga gtacgtggag aaatttcccc cgaaggcctc ggatgtttctg 180
gagatagatc ccgaggggga gaacataggc atagacgaca tcagaacgat aaaggacttc 240
ctgaactaca gccccgagct ctacacgaga aagtacgtga tagtccacga ctgtgaaaga 300
atgaccagc aggcggcgaa cgcgtttctg aaggcccttg aagaaccacc agaatacgct 360
gtgatcggtc tgaacactcg ccgctggcat tatctactgc cgacgataaa gagccgagtg 420
ttcagagtgg ttgtgaacgt tccaaaggag ttcagagatc tcgtgaaaga gaaaatagga 480
gatctctggg aggaacttcc acttcttgag agagacttca aaacggctct cgaagcctac 540
aaacttggtg cggaaaaact ttctggattg atggaaagtc tcaaagtttt ggagacggaa 600
aaactcttga aaaaggctct ttcaaaaggc ctcgaagggt atctcgcatg tagggagctc 660
ctggagagat tttcaaagggt ggaatcgaag gaattctttg cgctttttga tcaggtgact 720
aacacgataa caggaaaaga cgcgtttctt ttgatccaga gactgacaag aatcattctc 780
cacgaaaaca catgggaaag cgttgaagat caaaaaagcg tgtctttcct cgattcaatt 840
ctcaggttga agatagcgaa tctgaacaac aaactcactc tgatgaacat cctcgcgata 900
cacagagaga gaaagagagg tgtcaacgct tggagc 936
```

<210> 148

<211> 311

<212> PRT

<213> *Thermatoga maritima*

<400> 148

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Met Asn Asp Leu Ile Arg Lys Tyr Ala Lys Asp Gln Leu Glu Thr Leu
  1             5             10             15
```

```
Lys Arg Ile Ile Glu Lys Ser Glu Gly Ile Ser Ile Leu Ile Asn Gly
      20             25             30
```

```
Glu Asp Leu Ser Tyr Pro Arg Glu Val Ser Leu Glu Leu Pro Glu Tyr
      35             40             45
```

```
Val Glu Lys Phe Pro Pro Lys Ala Ser Asp Val Leu Glu Ile Asp Pro
      50             55             60
```

```
Glu Gly Glu Asn Ile Gly Ile Asp Asp Ile Arg Thr Ile Lys Asp Phe
      65             70             75             80
```

Leu Asn Tyr Ser Pro Glu Leu Tyr Thr Arg Lys Tyr Val Ile Val His
85 90 95

Asp Cys Glu Arg Met Thr Gln Gln Ala Ala Asn Ala Phe Leu Lys Ala
100 105 110

Leu Glu Glu Pro Pro Glu Tyr Ala Val Ile Val Leu Asn Thr Arg Arg
115 120 125

Trp His Tyr Leu Leu Pro Thr Ile Lys Ser Arg Val Phe Arg Val Val
130 135 140

Val Asn Val Pro Lys Glu Phe Arg Asp Leu Val Lys Glu Lys Ile Gly
145 150 155 160

Asp Leu Trp Glu Glu Leu Pro Leu Leu Glu Arg Asp Phe Lys Thr Ala
165 170 175

Leu Glu Ala Tyr Lys Leu Gly Ala Glu Lys Leu Ser Gly Leu Met Glu
180 185 190

Ser Leu Lys Val Leu Glu Thr Glu Lys Leu Leu Lys Lys Val Leu Ser
195 200 205

Lys Gly Leu Glu Gly Tyr Leu Ala Cys Arg Glu Leu Leu Glu Arg Phe
210 215 220

Ser Lys Val Glu Ser Lys Glu Phe Phe Ala Leu Phe Asp Gln Val Thr
225 230 235 240

Asn Thr Ile Thr Gly Lys Asp Ala Phe Leu Leu Ile Gln Arg Leu Thr
245 250 255

Arg Ile Ile Leu His Glu Asn Thr Trp Glu Ser Val Glu Asp Lys Ser
260 265 270

Val Ser Phe Leu Asp Ser Ile Leu Arg Val Lys Ile Ala Asn Leu Asn
275 280 285

Asn Lys Leu Thr Leu Met Asn Ile Leu Ala Ile His Arg Glu Arg Lys
290 295 300

Arg Gly Val Asn Ala Trp Ser
305 310

<210> 149

<211> 423
 <212> DNA
 <213> *Thermatoga maritima*

<400> 149
 atgtctttct tcaacaagat catactcata ggaagactcg tgagagatcc cgaagagaga 60
 tacacgctca gcggaactcc agtcaccacc ttcaccatag cggtaggacag gggtcccaga 120
 aagaacgcgc cggacgacgc tcaaacgact gattttcttca ggatcgtcac ctttggaaga 180
 ctggcagagt tcgctagaac ctatctcacc aaaggaaggc tcgttctcgt cgaaggtgaa 240
 atgagaatga gaagatggga aacaccact ggagaaaaga gggtagctcc ggaggttgtc 300
 gcaaacgttg ttagattcat ggacagaaaa cctgctgaaa cagtttagcga gactgaagag 360
 gagctggaaa taccggaaga agacttttcc agcgatacct tcagtgaaga tgaaccacca 420
 ttt 423

<210> 150
 <211> 141
 <212> PRT
 <213> *Thermatoga maritima*

<400> 150
 Met Ser Phe Phe Asn Lys Ile Ile Leu Ile Gly Arg Leu Val Arg Asp
 1 5 10 15
 Pro Glu Glu Arg Tyr Thr Leu Ser Gly Thr Pro Val Thr Thr Phe Thr
 20 25 30
 Ile Ala Val Asp Arg Val Pro Arg Lys Asn Ala Pro Asp Asp Ala Gln
 35 40 45
 Thr Thr Asp Phe Phe Arg Ile Val Thr Phe Gly Arg Leu Ala Glu Phe
 50 55 60
 Ala Arg Thr Tyr Leu Thr Lys Gly Arg Leu Val Leu Val Glu Gly Glu
 65 70 75 80
 Met Arg Met Arg Arg Trp Glu Thr Pro Thr Gly Glu Lys Arg Val Ser
 85 90 95
 Pro Glu Val Val Ala Asn Val Val Arg Phe Met Asp Arg Lys Pro Ala
 100 105 110
 Glu Thr Val Ser Glu Thr Glu Glu Glu Leu Glu Ile Pro Glu Glu Asp
 115 120 125
 Phe Ser Ser Asp Thr Phe Ser Glu Asp Glu Pro Pro Phe
 130 135 140

<210> 151
 <211> 1353
 <212> DNA
 <213> *Thermatoga maritima*

<400> 151
 atgctgtgttc ccccgacacaa cttagaggcc gaagttgctg tgctcggaag catattgata 60
 gatccgtcgg taataaacga cgttcttgaa attttgagcc acgaagattt ctatctgaaa 120
 aaacaccaac acatcttcag agcgatggaa gagctttacg acgaaggaaa accggtggac 180
 gtggtttccg tctgtgacaa gcttcaaagc atgggaaaac tcgaggaagt aggtggagat 240
 ctggaagtgg cccagctcgc tgaggctgtg cccagttctg cacacgcact tcactacgcg 300
 gagatcgtca aggaaaaatc cattctgagg aaactcattg agatctccag aaaaatctca 360
 gaaagtgcct acatggaaga agatgtggag atcctgctcg acaacgcaga aaagatgata 420
 ttcgagatct cagagatgaa aacgacaaaa tcctacgatc atctgagagg catcatgcac 480
 cgggtgtttg aaaacctgga gaacttcagg gaaagagcca accttataga acccggtgtg 540
 ctcataacgg gactaccaac gggattcaaa agtctggaca aacagaccac agggttccac 600
 agtccgatc tgggtgataat agcagcgaga ccctccatgg gaaaaacctc cttcgactc 660
 tcaatagcga ggaacatggc tgtcaatttc gaaatccccg tcggaatatt cagtctcgag 720
 atgtccaagg aacagctcgc tcaaagacta ctcagcatgg agtccggtgt ggatctttac 780
 agcatcagaa caggatacct ggatcaggag aagtgggaaa gactcacaat agcggcttct 840
 aaactctaca aagcaccat agttgtggac gatgagtcac tcctcgatcc gcgatcgttg 900
 agggcaaaaag cgagaaggat gaaaaaagaa tacgatgtaa aagccatttt tgctgactat 960
 ctccagctca tgcacctgaa aggaagaaaa gaaagcagac agcaggagat atccgagatc 1020
 tcgagatctc tgaagctcct tgcgagggaa ctcgacatag tggatgtagc gctttcacag 1080
 ctttcgaggg ccgtagaaca gagagaagac aaaagaccga ggctgagtga cctcagggaa 1140
 tccggtgcga tagaacagga cgcagacaca gtcattctca tctacaggga ggaatattac 1200
 aggagcaaaa aatccaaaga ggaaagcaag cttcacgaac ctcacgaagc tgaaatcata 1260
 ataggtaaac agagaaacgg tcccgttgga acgatcactc tgatcttcga cccagaacg 1320
 gttacgttcc atgaagtcga tgtggtgcat tca 1353

<210> 152
 <211> 451
 <212> PRT
 <213> *Thermatoga maritima*

<400> 152
 Met Arg Val Pro Pro His Asn Leu Glu Ala Glu Val Ala Val Leu Gly
 1 5 10 15
 Ser Ile Leu Ile Asp Pro Ser Val Ile Asn Asp Val Leu Glu Ile Leu
 20 25 30
 Ser His Glu Asp Phe Tyr Leu Lys Lys His Gln His Ile Phe Arg Ala
 35 40 45
 Met Glu Glu Leu Tyr Asp Glu Gly Lys Pro Val Asp Val Val Ser Val

50		55		60	
Cys Asp Lys Leu Gln Ser Met Gly Lys Leu Glu Glu Val Gly Gly Asp					
65		70		75	80
Leu Glu Val Ala Gln Leu Ala Glu Ala Val Pro Ser Ser Ala His Ala					
	85		90		95
Leu His Tyr Ala Glu Ile Val Lys Glu Lys Ser Ile Leu Arg Lys Leu					
	100		105		110
Ile Glu Ile Ser Arg Lys Ile Ser Glu Ser Ala Tyr Met Glu Glu Asp					
	115		120		125
Val Glu Ile Leu Leu Asp Asn Ala Glu Lys Met Ile Phe Glu Ile Ser					
	130		135		140
Glu Met Lys Thr Thr Lys Ser Tyr Asp His Leu Arg Gly Ile Met His					
145		150		155	160
Arg Val Phe Glu Asn Leu Glu Asn Phe Arg Glu Arg Ala Asn Leu Ile					
	165		170		175
Glu Pro Gly Val Leu Ile Thr Gly Leu Pro Thr Gly Phe Lys Ser Leu					
	180		185		190
Asp Lys Gln Thr Thr Gly Phe His Ser Ser Asp Leu Val Ile Ile Ala					
	195		200		205
Ala Arg Pro Ser Met Gly Lys Thr Ser Phe Ala Leu Ser Ile Ala Arg					
	210		215		220
Asn Met Ala Val Asn Phe Glu Ile Pro Val Gly Ile Phe Ser Leu Glu					
225		230		235	240
Met Ser Lys Glu Gln Leu Ala Gln Arg Leu Leu Ser Met Glu Ser Gly					
	245		250		255
Val Asp Leu Tyr Ser Ile Arg Thr Gly Tyr Leu Asp Gln Glu Lys Trp					
	260		265		270
Glu Arg Leu Thr Ile Ala Ala Ser Lys Leu Tyr Lys Ala Pro Ile Val					
	275		280		285
Val Asp Asp Glu Ser Leu Leu Asp Pro Arg Ser Leu Arg Ala Lys Ala					
	290		295		300
Arg Arg Met Lys Lys Glu Tyr Asp Val Lys Ala Ile Phe Val Asp Tyr					


```

aaaaaagtgg caaaagaggt tgggttttttc gtcacccaccg aaggctactt cgacgcgctc 780
gcattcagaa aggatggaat accaacggcg gtcgctgttc ttggggcgag tctttcaaga 840
gaggcgattc taaaactttc ggcgtattcg aaaaacgtca tactgtgttt cgataatgac 900
aaagcaggct tcagagccac tctcaaattcc ctcgaggatc tcctagacta cgaattcaac 960
gtgcttgtgg caacccccctc tccttacaaa gaccagatg aactctttca gaaagaagga 1020
gaaggttcat tgaaaaagat gctgaaaaaac tcgcttcgt tcgaatattt tctggtgacg 1080
gctggtgagg tcttctttga caggaacagc cccgcgggtg tgagatccta ctttctttc 1140
ctcaaagggt ggggtccaaa gatgagaagg aaaggatatt tgaaacacat agaaaatctc 1200
gtgaatgagg tttcatcttc tctccagata ccagaaaacc agattttgaa cttttttgaa 1260
agcgacaggt ctaacactat gcctgttcat gagaccaagt cgtcaaagggt ttacgatgag 1320
gggagaggac tggcttattt gtttttgaac tacgaggatt tgagggaaaa gattctggaa 1380
ctggacttag aggtactgga agataaaaac gcgagggagt ttttcaagag agtctcactg 1440
ggagaagatt tgaacaaagt catagaaaac ttcccaaaag agctgaaaga ctggattttt 1500
gagacaatag aaagcattcc tcctccaaag gatcccgaga aattcctcgg tgacctctcc 1560
gaaaagttga aaatccgacg gatagagaga cgtatcgag aaatagatga tatgataaag 1620
aaagcttcaa acgatgaaga aaggcgtctt cttctctcta tgaaagtgga tctctcaga 1680
aaaataaaga ggagg 1695

```

<210> 154

<211> 565

<212> PRT

<213> *Thermatoga maritima*

<400> 154

```

Met Ile Pro Arg Glu Val Ile Glu Glu Ile Lys Glu Lys Val Asp Ile
  1             5             10             15

```

```

Val Glu Val Ile Ser Glu Tyr Val Asn Leu Thr Arg Val Gly Ser Ser
          20             25             30

```

```

Tyr Arg Ala Leu Cys Pro Phe His Ser Glu Thr Asn Pro Ser Phe Tyr
      35             40             45

```

```

Val His Pro Gly Leu Lys Ile Tyr His Cys Phe Gly Cys Gly Ala Ser
      50             55             60

```

```

Gly Asp Val Ile Lys Phe Leu Gln Glu Met Glu Gly Ile Ser Phe Gln
      65             70             75             80

```

```

Glu Ala Leu Glu Arg Leu Ala Lys Arg Ala Gly Ile Asp Leu Ser Leu
          85             90             95

```

```

Tyr Arg Thr Glu Gly Thr Ser Glu Tyr Gly Lys Tyr Ile Arg Leu Tyr
      100            105            110

```

```

Glu Glu Thr Trp Lys Arg Tyr Val Lys Glu Leu Glu Lys Ser Lys Glu
      115            120            125

```

Ala	Lys	Asp	Tyr	Leu	Lys	Ser	Arg	Gly	Phe	Ser	Glu	Glu	Asp	Ile	Ala	
130						135					140					
Lys	Phe	Gly	Phe	Gly	Tyr	Val	Pro	Lys	Arg	Ser	Ser	Ile	Ser	Ile	Glu	
145					150					155					160	
Val	Ala	Glu	Gly	Met	Asn	Ile	Thr	Leu	Glu	Glu	Leu	Val	Arg	Tyr	Gly	
				165					170					175		
Ile	Ala	Leu	Lys	Lys	Gly	Asp	Arg	Phe	Val	Asp	Arg	Phe	Glu	Gly	Arg	
			180					185					190			
Ile	Val	Val	Pro	Ile	Lys	Asn	Asp	Ser	Gly	His	Ile	Val	Ala	Phe	Gly	
		195					200					205				
Gly	Arg	Ala	Leu	Gly	Asn	Glu	Glu	Pro	Lys	Tyr	Leu	Asn	Ser	Pro	Glu	
	210					215					220					
Thr	Arg	Tyr	Phe	Ser	Lys	Lys	Lys	Thr	Leu	Phe	Leu	Phe	Asp	Glu	Ala	
225					230					235					240	
Lys	Lys	Val	Ala	Lys	Glu	Val	Gly	Phe	Phe	Val	Ile	Thr	Glu	Gly	Tyr	
				245					250					255		
Phe	Asp	Ala	Leu	Ala	Phe	Arg	Lys	Asp	Gly	Ile	Pro	Thr	Ala	Val	Ala	
		260						265					270			
Val	Leu	Gly	Ala	Ser	Leu	Ser	Arg	Glu	Ala	Ile	Leu	Lys	Leu	Ser	Ala	
		275					280					285				
Tyr	Ser	Lys	Asn	Val	Ile	Leu	Cys	Phe	Asp	Asn	Asp	Lys	Ala	Gly	Phe	
	290					295					300					
Arg	Ala	Thr	Leu	Lys	Ser	Leu	Glu	Asp	Leu	Leu	Asp	Tyr	Glu	Phe	Asn	
305					310					315					320	
Val	Leu	Val	Ala	Thr	Pro	Ser	Pro	Tyr	Lys	Asp	Pro	Asp	Glu	Leu	Phe	
				325					330					335		
Gln	Lys	Glu	Gly	Glu	Gly	Ser	Leu	Lys	Lys	Met	Leu	Lys	Asn	Ser	Arg	
			340					345					350			
Ser	Phe	Glu	Tyr	Phe	Leu	Val	Thr	Ala	Gly	Glu	Val	Phe	Phe	Asp	Arg	
		355					360					365				
Asn	Ser	Pro	Ala	Gly	Val	Arg	Ser	Tyr	Leu	Ser	Phe	Leu	Lys	Gly	Trp	
	370					375					380					

Val Gln Lys Met Arg Arg Lys Gly Tyr Leu Lys His Ile Glu Asn Leu
 385 390 395 400

Val Asn Glu Val Ser Ser Ser Leu Gln Ile Pro Glu Asn Gln Ile Leu
 405 410 415

Asn Phe Phe Glu Ser Asp Arg Ser Asn Thr Met Pro Val His Glu Thr
 420 425 430

Lys Ser Ser Lys Val Tyr Asp Glu Gly Arg Gly Leu Ala Tyr Leu Phe
 435 440 445

Leu Asn Tyr Glu Asp Leu Arg Glu Lys Ile Leu Glu Leu Asp Leu Glu
 450 455 460

Val Leu Glu Asp Lys Asn Ala Arg Glu Phe Phe Lys Arg Val Ser Leu
 465 470 475 480

Gly Glu Asp Leu Asn Lys Val Ile Glu Asn Phe Pro Lys Glu Leu Lys
 485 490 495

Asp Trp Ile Phe Glu Thr Ile Glu Ser Ile Pro Pro Pro Lys Asp Pro
 500 505 510

Glu Lys Phe Leu Gly Asp Leu Ser Glu Lys Leu Lys Ile Arg Arg Ile
 515 520 525

Glu Arg Arg Ile Ala Glu Ile Asp Asp Met Ile Lys Lys Ala Ser Asn
 530 535 540

Asp Glu Glu Arg Arg Leu Leu Leu Ser Met Lys Val Asp Leu Leu Arg
 545 550 555 560

Lys Ile Lys Arg Arg
 565

<210> 155

<211> 804

<212> DNA

<213> Thermus thermophilus

<400> 155

atggctctac acccggctca ccctggggca ataatcgggc acgaggccgt tctcgccctc 60
 ctccccgcc tcaccgccca gaccctgctc ttctccggcc ccgagggggg ggggcggcgc 120
 accgtggccc gctggtacgc ctgggggctc aaccgcggct tccccccgcc ctccctgggg 180
 gagcaccogg acgtcctcga ggtggggccc aaggcccggg acctccgggg ccgggccgag 240

gtgcggtggtg aggaggtggc gcccctcttg gagtgggtgct ccagccaccc ccgggagcgg 300
 gtgaaggtgg ccacccctgga ctcgccccac ctctcaccg aggcgcgcgc caacgccttc 360
 ctcaagctcc tggaggagcc ccttcctac gcccgcatcg tctcatcgc cccaagccgc 420
 gccaccctcc tccccaccct ggccctccgg gccacggagg tggcattcgc ccccggtgcc 480
 gaggaggccc tgcgcgcct caccaggac ccggagctcc tccgctacgc cgcgggggcc 540
 ccgggcgcgc tccttagggc cctccaggac ccggaggggt accgggccc catggccagg 600
 gcgcaaaggg tcctgaaagc cccgcccctg gagcgctcg ctttgcttcg ggagcttttg 660
 gccgaggagg aggggggtcca cgcctccac gccgtcctaa agcgcgcgga gcacctcctt 720
 gccctggagc gggcgcgga ggcctggag gggtagctga gcccagagct ggtcctcgcc 780
 cggctggcct tagacttaga gaca 804

<210> 156

<211> 268

<212> PRT

<213> *Thermus thermophilus*

<400> 156

Met	Ala	Leu	His	Pro	Ala	His	Pro	Gly	Ala	Ile	Ile	Gly	His	Glu	Ala	1	5	10	15
Val	Leu	Ala	Leu	Leu	Pro	Arg	Leu	Thr	Ala	Gln	Thr	Leu	Leu	Phe	Ser	20	25	30	
Gly	Pro	Glu	Gly	Val	Gly	Arg	Arg	Thr	Val	Ala	Arg	Trp	Tyr	Ala	Trp	35	40	45	
Gly	Leu	Asn	Arg	Gly	Phe	Pro	Pro	Pro	Ser	Leu	Gly	Glu	His	Pro	Asp	50	55	60	
Val	Leu	Glu	Val	Gly	Pro	Lys	Ala	Arg	Asp	Leu	Arg	Gly	Arg	Ala	Glu	65	70	75	80
Val	Arg	Leu	Glu	Glu	Val	Ala	Pro	Leu	Leu	Glu	Trp	Cys	Ser	Ser	His	85	90	95	
Pro	Arg	Glu	Arg	Val	Lys	Val	Ala	Ile	Leu	Asp	Ser	Ala	His	Leu	Leu	100	105	110	
Thr	Glu	Ala	Ala	Ala	Asn	Ala	Leu	Leu	Lys	Leu	Leu	Glu	Glu	Pro	Pro	115	120	125	
Ser	Tyr	Ala	Arg	Ile	Val	Leu	Ile	Ala	Pro	Ser	Arg	Ala	Thr	Leu	Leu	130	135	140	
Pro	Thr	Leu	Ala	Ser	Arg	Ala	Thr	Glu	Val	Ala	Phe	Ala	Pro	Val	Pro	145	150	155	160

Glu Glu Ala Leu Arg Ala Leu Thr Gln Asp Pro Glu Leu Leu Arg Tyr
165 170 175

Ala Ala Gly Ala Pro Gly Arg Leu Leu Arg Ala Leu Gln Asp Pro Glu
180 185 190

Gly Tyr Arg Ala Arg Met Ala Arg Ala Gln Arg Val Leu Lys Ala Pro
195 200 205

Pro Leu Glu Arg Leu Ala Leu Leu Arg Glu Leu Leu Ala Glu Glu Glu
210 215 220

Gly Val His Ala Leu His Ala Val Leu Lys Arg Pro Glu His Leu Leu
225 230 235 240

Ala Leu Glu Arg Ala Arg Glu Ala Leu Glu Gly Tyr Val Ser Pro Glu
245 250 255

Leu Val Leu Ala Arg Leu Ala Leu Asp Leu Glu Thr
260 265

<210> 157
<211> 729
<212> DNA
<213> Thermus thermophilus

<400> 157
atgctggacc tgagggaggt gggggaggcg gagggaagg ccctaaagcc ctttttggaa 60
agcgtgcccg agggcgcccc cgctcctcctc ctggacccta agccaagccc ctcccgggcg 120
gccttctacc ggaaccggga aaggcgggac ttccccaccc ccaaggggaa ggacctggtg 180
cggcacctgg aaaaccgggc caagcgccctg gggctcaggc tcccgggagg ggtggcccag 240
tacctggcct ccctggaggg ggacctcgag gccctggagc gggagctgga gaagcttgcc 300
ctcctctccc caccctcac cctggagaag gtggagaagg tgggtggccct gaggcccccc 360
ctcacgggct ttgacctggt gcgctccgctc ctggagaagg accccaagga ggccctcctg 420
cgcctaggcg gcctcaagga ggagggggag gagccctca ggctcctcgg ggccctctcc 480
tggcagttcg ccctcctcgc ccgggccttc ttctcctcc gggaaaacc caggcccaag 540
gaggaggacc tcgcccgcct cgaggccac ccctacgccg ccgcccgcgc cctggaggcg 600
gcgaagcgcc tcacggaaga ggccctcaag gaggccctgg acgcctcat ggaggcgga 660
aagagggcca agggggggaa agaccctgg ctcgccctgg aggcggcggt cctccgcctc 720
gcccgttga 729

<210> 158
<211> 292
<212> PRT
<213> Thermus thermophilus

<400> 158

Met Val Ile Ala Phe Thr Gly Asp Pro Phe Leu Ala Arg Glu Ala Leu
1 5 10 15

Leu Glu Glu Ala Arg Leu Arg Gly Leu Ser Arg Phe Thr Glu Pro Thr
20 25 30

Pro Glu Ala Leu Ala Gln Ala Leu Ala Pro Gly Leu Phe Gly Gly Gly
35 40 45

Gly Ala Met Leu Asp Leu Arg Glu Val Gly Glu Ala Glu Trp Lys Ala
50 55 60

Leu Lys Pro Leu Leu Glu Ser Val Pro Glu Gly Val Pro Val Leu Leu
65 70 75 80

Leu Asp Pro Lys Pro Ser Pro Ser Arg Ala Ala Phe Tyr Arg Asn Arg
85 90 95

Glu Arg Arg Asp Phe Pro Thr Pro Lys Gly Lys Asp Leu Val Arg His
100 105 110

Leu Glu Asn Arg Ala Lys Arg Leu Gly Leu Arg Leu Pro Gly Gly Val
115 120 125

Ala Gln Tyr Leu Ala Ser Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg
130 135 140

Glu Leu Glu Lys Leu Ala Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys
145 150 155 160

Val Glu Lys Val Val Ala Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu
165 170 175

Val Arg Ser Val Leu Glu Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu
180 185 190

Gly Gly Leu Lys Glu Glu Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala
195 200 205

Leu Ser Trp Gln Phe Ala Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg
210 215 220

Glu Asn Pro Arg Pro Lys Glu Glu Asp Leu Ala Arg Leu Glu Ala His
225 230 235 240

Pro Tyr Ala Ala Arg Arg Ala Leu Glu Ala Ala Lys Arg Leu Thr Glu
245 250 255

Glu Ala Leu Lys Glu Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg
260 265 270

Ala Lys Gly Gly Lys Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu
275 280 285

Arg Leu Ala Arg
290

<210> 159
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 159
gtgtgtcata tgagtaagga ttctgtccac cttcacc 37

<210> 160
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 160
gtgtgtggat ccgggggacta ctcggaagta aggg 34

<210> 161
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 161
gtgtgtcata tggaaaccac aatattccag ttccag 36

<210> 162

<211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 162
 gtgtgtggat ccttatccac catgagaagt atttttcac 39

 <210> 163
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 163
 gtgtgtcata tggaaaaagt tttttttgga aaaaactcca g 41

 <210> 164
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 164
 gtgtgtggat ccttaatccg cctgaacggc taacg 35

 <210> 165
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: primer

 <400> 165
 gtgtgtcata tgaactacgt tcccttcgag agaaagtaca g 41

 <210> 166

<211> 36
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 166
gtgtgtggat ccttaaaaca gcctcgtccc gctgga 36

<210> 167
<211> 33
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 167
gtgtgtcata tgcgcgttaa ggtggacagg gag 33

<210> 168
<211> 35
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 168
tgtgtctcga gtcatggcta caccctcatc ggcac 35

<210> 169
<211> 47
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 169
gtgtgtcata tgctcaataa ggtttttata ataggaagac ttacggg 47

<210> 170

<211> 39
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 170
gtgtggatcc ttaaaaaggt atttcgtcct cttcatcgg 39

<210> 171
<211> 807
<212> DNA
<213> Thermus thermophilus

<400> 171
atggctcgag gcctgaaccg cgttttcctc atcggcgccc tcgccaccgg gccggacatg 60
cgctacaccc cggcgggggt cgccattttg gacctgacct tcgccgggtca ggacctgctt 120
ctttccgata acggggggga accggaggtg tcctgggtacc accgggtgag gctcttaggc 180
cgccaggcgg agatgtgggg cgacctcttg gaccaagggc agctcgtctt cgtggagggc 240
cgcttgaggt accgccagtg ggaaaggagg ggggagaagc ggagcgagct ccagatccgg 300
gccgacttcc ggacccccctg gacgaccggg ggaagaagcg ggcggaggac agccggggcc 360
agcccagggt ccgcgcgcgc ctgaaccagg tcttcctcat gggcaacctg acccggggacc 420
cggaactccg ctacaccccc cagggcaccg cggtgggccc gctgggcctg gcggtgaacg 480
agcgcgcgcca gggggcggag gagcgcaccc acttcgtgga ggttcaggcc tggcgcgacc 540
tggcggagtg ggccgcggag ctgaggaagg gcgacggcct tttcgtgatc ggcaggttgg 600
tgaacgactc ctggaccagc tccagcggcg agcggcgctt ccagaccggt gtggaggccc 660
tcaggctgga gcgccccacc cgtggacctg cccaggcctg cccaggccgg cggaacaggt 720
cccgcgaagt ccagacgggt ggggtggaca ttgacgaagg cttggaagac tttccggcgg 780
aggaggattt gccgttttga gcacgaa 807

<210> 172
<211> 266
<212> PRT
<213> Thermus thermophilus

<400> 172
Met Ala Arg Gly Leu Asn Arg Val Phe Leu Ile Gly Ala Leu Ala Thr
1 5 10 15
Arg Pro Asp Met Arg Tyr Thr Pro Ala Gly Leu Ala Ile Leu Asp Leu
20 25 30
Thr Leu Ala Gly Gln Asp Leu Leu Leu Ser Asp Asn Gly Gly Glu Pro
35 40 45

Glu Val Ser Trp Tyr His Arg Val Arg Leu Leu Gly Arg Gln Ala Glu
50 55 60

Met Trp Gly Asp Leu Leu Asp Gln Gly Gln Leu Val Phe Val Glu Gly
65 70 75 80

Arg Leu Glu Tyr Arg Gln Trp Glu Arg Glu Gly Glu Lys Arg Ser Glu
85 90 95

Leu Gln Ile Arg Ala Asp Phe Leu Asp Pro Leu Asp Asp Arg Gly Lys
100 105 110

Lys Arg Ala Glu Asp Ser Arg Gly Gln Pro Arg Leu Arg Ala Ala Leu
115 120 125

Asn Gln Val Phe Leu Met Gly Asn Leu Thr Arg Asp Pro Glu Leu Arg
130 135 140

Tyr Thr Pro Gln Gly Thr Ala Val Ala Arg Leu Gly Leu Ala Val Asn
145 150 155 160

Glu Arg Arg Gln Gly Ala Glu Glu Arg Thr His Phe Val Glu Val Gln
165 170 175

Ala Trp Arg Asp Leu Ala Glu Trp Ala Ala Glu Leu Arg Lys Gly Asp
180 185 190

Gly Leu Phe Val Ile Gly Arg Leu Val Asn Asp Ser Trp Thr Ser Ser
195 200 205

Ser Gly Glu Arg Arg Phe Gln Thr Arg Val Glu Ala Leu Arg Leu Glu
210 215 220

Arg Pro Thr Arg Gly Pro Ala Gln Ala Cys Pro Gly Arg Arg Asn Arg
225 230 235 240

Ser Arg Glu Val Gln Thr Gly Gly Val Asp Ile Asp Glu Gly Leu Glu
245 250 255

Asp Phe Pro Pro Glu Glu Asp Leu Pro Phe
260 265

<210> 173

<211> 992

<212> DNA

<213> Bacillus stearothermophilus

<400> 173

```
aattccgaca tttcaattga atcgtttatt ccgcttgaaa aagaaggcaa gttgctcggtt 60
gatgtgaaaa gaccggggag catcgtactg caggcgcgct ttttctctga aatcgtgaaa 120
aaactgccgc aacaaacggt ggaaatcgaa acggaagaca actttttgac gatcatccgc 180
tcggggcact cagaattccg cctcaatggg ctaaacgccg acgaatatcc gcgcctgccg 240
caaattgaag aagaaaacgt gtttcaaata ccggctgatt tattgaaaac cgtgattcgg 300
caaacggtgt tcgccgtttc tacatcgga aacgcgccaa tcttgacagg tgtcaactgg 360
aaagtgaac atggcgagct tgtctgcaca gcgaccgaca gtcacgcgtt agccatgcgc 420
aaagtgaaaa ttgagtcgga aaatgaagta tcatacaacg tcgtcatccc tggaaaaagt 480
cttaatgagc tcagcaaaat tttggatgac ggcaaccacc cgggtggacat cgtcatgaca 540
gccaatcaag tgctatttaa ggccgagcac cttctcttct tttcccggtt gcttgacggc 600
aactatccgg agacggcccg cttgattcca acagaaagca aaacgaccat gatcgtcaat 660
gcaaaagagt ttctgcaggc aatcgaccga gcgtccttgc ttgctcgaga aggaaggaac 720
aacgttgtga aactgacgac gcttctctgga ggaatgctcg aaatttcttc gatttctccg 780
agatcgggaa agtgacggag cagctgcaaa cggagtctct tgaaggggaa gagttgaaca 840
tttcgttcag cgcgaaatat atgatggacg cgttgccggc gcttgatgga acagacattt 900
caaatcagct tcaactggggc catgcggccg ttctgtttgc gcccggttca accgattcga 960
tgcttcagct ctttttggcg gtgagaacat at 992
```

<210> 174

<211> 334

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 174

```
Asn Ser Asp Ile Ser Ile Ile Glu Ser Phe Ile Pro Leu Glu Lys Glu
 1             5             10             15

Gly Lys Leu Leu Val Asp Val Lys Arg Pro Gly Ser Ile Val Leu Gln
      20             25             30

Ala Arg Phe Phe Ser Glu Ile Val Lys Lys Leu Pro Gln Gln Thr Val
      35             40             45

Glu Ile Glu Thr Glu Asp Asn Phe Leu Thr Ile Ile Arg Ser Gly His
      50             55             60

Ser Glu Phe Arg Leu Asn Gly Leu Asn Ala Asp Glu Tyr Pro Arg Leu
      65             70             75             80

Pro Gln Ile Glu Glu Glu Asn Val Phe Gln Ile Pro Ala Asp Leu Leu
      85             90             95

Lys Thr Val Ile Arg Gln Thr Val Phe Ala Val Ser Thr Ser Glu Thr
      100            105            110

Arg Pro Ile Leu Thr Gly Val Asn Trp Lys Val Glu His Gly Glu Leu
```

115					120					125					
Val	Cys	Thr	Ala	Thr	Asp	Ser	His	Arg	Leu	Ala	Met	Arg	Lys	Val	Lys
130						135					140				
Ile	Ile	Glu	Ser	Glu	Asn	Glu	Val	Ser	Tyr	Asn	Val	Val	Ile	Pro	Gly
145					150					155					160
Lys	Ser	Leu	Asn	Glu	Leu	Ser	Lys	Ile	Ile	Leu	Asp	Asp	Gly	Asn	His
				165					170					175	
Pro	Val	Asp	Ile	Val	Met	Thr	Ala	Asn	Gln	Val	Leu	Phe	Lys	Ala	Glu
			180					185					190		
His	Leu	Leu	Phe	Phe	Ser	Arg	Leu	Leu	Asp	Gly	Asn	Tyr	Pro	Glu	Thr
	195						200					205			
Ala	Arg	Leu	Ile	Pro	Thr	Glu	Ser	Lys	Thr	Thr	Met	Ile	Val	Asn	Ala
	210					215					220				
Lys	Glu	Phe	Leu	Gln	Ala	Ile	Asp	Arg	Ala	Ser	Leu	Leu	Ala	Arg	Glu
225				230						235					240
Gly	Arg	Asn	Asn	Val	Val	Lys	Leu	Thr	Thr	Leu	Pro	Gly	Gly	Met	Leu
			245					250						255	
Glu	Ile	Ser	Ser	Ile	Ser	Pro	Glu	Ile	Gly	Lys	Val	Thr	Glu	Gln	Leu
		260						265					270		
Gln	Thr	Glu	Ser	Leu	Glu	Gly	Glu	Glu	Leu	Asn	Ile	Ser	Phe	Ser	Ala
		275					280					285			
Lys	Tyr	Met	Met	Asp	Ala	Leu	Arg	Ala	Leu	Asp	Gly	Thr	Asp	Ile	Gln
	290					295					300				
Ile	Ser	Phe	Thr	Gly	Ala	Met	Arg	Pro	Phe	Leu	Leu	Arg	Pro	Leu	His
305					310					315					320
Thr	Asp	Ser	Met	Leu	Gln	Leu	Ile	Leu	Pro	Val	Arg	Thr	Tyr		
			325					330							

<210> 175
 <211> 492
 <212> DNA
 <213> *Bacillus stearothermophilus*

 <400> 175

```

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ccaagcggag tggctgttgc cacgtttacg ctgcggtca accgtccgtt tacaaatcag 120
cagggcgagc gggaaacgga ttttattcaa tgtgtcgttt ggcgccgcca ggcggaaaac 180
gtcgccaact ttttgaaaaa ggggagcttg gctggtgtcg atggccgact gcaaaccgc 240
agctatgaaa atcaagaagg tcggcgtgtg tacgtgacgg aagtgggtggc tgatagcgtc 300
caatttcttg agccgaaagg aacgagcgag cagcgagggg cgacagcagg cggctactat 360
ggggatccat tcccattcgg gcaagatcag aaccaccaat atccgaacga aaaagggttt 420
ggccgcacgc atgacgatcc tttcgccaat gacggccagc cgatcgatat ttctgatgat 480
gatttgccgt tt 492

```

<210> 176

<211> 164

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 176

```

Met Ile Asn Arg Val Ile Leu Val Gly Arg Leu Thr Arg Asp Pro Glu
  1             5             10             15

```

```

Leu Arg Tyr Thr Pro Ser Gly Val Ala Val Ala Thr Phe Thr Leu Ala
          20             25             30

```

```

Val Asn Arg Pro Phe Thr Asn Gln Ser Tyr Glu Asn Gln Glu Gly Arg
          35             40             45

```

```

Arg Val Tyr Val Thr Glu Val Val Ala Asp Ser Val Gln Phe Leu Glu
          50             55             60

```

```

Pro Lys Gly Thr Ser Glu Gln Arg Gly Ala Thr Ala Gly Gly Tyr Tyr
          65             70             75             80

```

```

Gln Gly Glu Arg Glu Thr Asp Phe Ile Gln Cys Val Val Trp Arg Arg
          85             90             95

```

```

Gln Ala Glu Asn Val Ala Asn Phe Leu Lys Lys Gly Ser Leu Ala Gly
          100            105            110

```

```

Val Asp Gly Arg Leu Gln Thr Arg Gly Asp Pro Phe Pro Phe Gly Gln
          115            120            125

```

```

Asp Gln Asn His Gln Tyr Pro Asn Glu Lys Gly Phe Gly Arg Ile Asp
          130            135            140

```

```

Asp Asp Pro Phe Ala Asn Asp Gly Gln Pro Ile Asp Ile Ser Asp Asp
          145            150            155            160

```

Asp Leu Pro Phe

<210> 177
 <211> 1044
 <212> DNA
 <213> Bacillus stearothermophilus

<400> 177
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 tacggcaatg agccgttttt attaacggaa acgtatgagc gattggtgaa cgcagcgctt 120
 ggccccgagg agcgggagtg gaacttggct gtgtacgact gcgaggaaac gccgatcgag 180
 gcggcgcttg aggaggccga gacggtgccg ttttcggcg agcggcggtgt cattctcatc 240
 aagcatccat atttttttac gtctgaaaaa gagaaggaga tcgaacatga tttggcgaag 300
 ctggaggcgt acttgaaggc gccgtcgccg ttttcgatcg tcgtcttttt cgcgccgtac 360
 gagaagcttg atgagcgaaa aaaaattacg aagctcgcca aagagcaaag cgaagtcgtc 420
 atcgccgccc cgctcgccga agcggagctg cgtgcctggg tgcggcgccg catcgagagc 480
 caaggggccc aagcaagcga cgaggcgatt gatgtcctgt tgcggcgggc cgggacgcag 540
 ctttcgcctt tggcgaatga aatcgataaa ttggccctgt ttgccggatc gggcggaacc 600
 atcgaggcgg cggcggttga gcggcttgct gcccgcacgc cggaagaaaa cgtatttgtg 660
 cttgtcgagc aagtggcgaa gcgcgacatt ccagcagcgt tgcagacgtt ttatgatctg 720
 cttgaaaaca atgaagagcc gatcaaaatt ttggcggttg tcgccgcca tttccgcttg 780
 ctttcgcaag tgaaatggct tgcctcctta ggctacggac aggcgcaaatt tgctgcggcg 840
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 ggagagcttg ctgaggcgat caacgagctc gctgacgccg attacgaagt gaaaagcggg 960
 gcggtcgacg gccggttggc cggttgagctg cttctgatgc gctggggcgc ccgccccggc 1020
 caagcggggc gccacggccg gcgg 1044

<210> 178
 <211> 348
 <212> PRT
 <213> Bacillus stearothermophilus

<400> 178
 Met Leu Glu Arg Val Trp Gly Asn Ile Glu Lys Arg Arg Phe Ser Pro
 1 5 10 15
 Leu Tyr Leu Leu Tyr Gly Asn Glu Pro Phe Leu Leu Thr Glu Thr Tyr
 20 25 30
 Glu Arg Leu Val Asn Ala Ala Leu Gly Pro Glu Glu Arg Glu Trp Asn
 35 40 45
 Leu Ala Val Tyr Asp Cys Glu Glu Thr Pro Ile Glu Ala Ala Leu Glu
 50 55 60
 Glu Ala Glu Thr Val Pro Phe Phe Gly Glu Arg Arg Val Ile Leu Ile

65					70					75					80
Lys	His	Pro	Tyr	Phe	Phe	Thr	Ser	Glu	Lys	Glu	Lys	Glu	Ile	Glu	His
				85					90					95	
Asp	Leu	Ala	Lys	Leu	Glu	Ala	Tyr	Leu	Lys	Ala	Pro	Ser	Pro	Phe	Ser
			100					105					110		
Ile	Val	Val	Phe	Phe	Ala	Pro	Tyr	Glu	Lys	Leu	Asp	Glu	Arg	Lys	Lys
		115					120					125			
Ile	Thr	Lys	Leu	Ala	Lys	Glu	Gln	Ser	Glu	Val	Val	Ile	Ala	Ala	Pro
	130					135					140				
Leu	Ala	Glu	Ala	Glu	Leu	Arg	Ala	Trp	Val	Arg	Arg	Arg	Ile	Glu	Ser
145					150					155					160
Gln	Gly	Ala	Gln	Ala	Ser	Asp	Glu	Ala	Ile	Asp	Val	Leu	Leu	Arg	Arg
			165						170					175	
Ala	Gly	Thr	Gln	Leu	Ser	Ala	Leu	Ala	Asn	Glu	Ile	Asp	Lys	Leu	Ala
		180					185					190			
Leu	Phe	Ala	Gly	Ser	Gly	Gly	Thr	Ile	Glu	Ala	Ala	Ala	Val	Glu	Arg
	195						200					205			
Leu	Val	Ala	Arg	Thr	Pro	Glu	Glu	Asn	Val	Phe	Val	Leu	Val	Glu	Gln
	210					215					220				
Val	Ala	Lys	Arg	Asp	Ile	Pro	Ala	Ala	Leu	Gln	Thr	Phe	Tyr	Asp	Leu
225					230					235					240
Leu	Glu	Asn	Asn	Glu	Glu	Pro	Ile	Lys	Ile	Leu	Ala	Leu	Leu	Ala	Ala
			245						250					255	
His	Phe	Arg	Leu	Leu	Ser	Gln	Val	Lys	Trp	Leu	Ala	Ser	Leu	Gly	Tyr
		260						265					270		
Gly	Gln	Ala	Gln	Ile	Ala	Ala	Ala	Leu	Lys	Val	His	Pro	Phe	Arg	Val
	275						280					285			
Lys	Leu	Ala	Leu	Ala	Gln	Ala	Ala	Arg	Phe	Ala	Asp	Gly	Glu	Leu	Ala
	290					295					300				
Glu	Ala	Ile	Asn	Glu	Leu	Ala	Asp	Ala	Asp	Tyr	Glu	Val	Lys	Ser	Gly
305					310					315					320
Ala	Val	Asp	Arg	Arg	Leu	Ala	Val	Glu	Leu	Leu	Leu	Met	Arg	Trp	Gly

325

330

335

Ala Arg Pro Ala Gln Ala Gly Arg His Gly Arg Arg
 340 - - - 345 -

<210> 179

<211> 757

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 179

```

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aaagcggcca gtttggttgtt ggcgaaacgt ttgttttgtc tgtccccaat cggagtttcc 180
ccgtgtctag agtgccgcaa ctgccggcgc atcgactccg gcaaccaccc tgacgtccgg 240
gtgatcggcc cagatggagg atcaatcaaa aaggaacaaa tcgaatggct gcagcaagag 300
ttctcgaaaa cagcggctga gtcggataaa aaaatgtaca tcgttgagca cgccgatcaa 360
atgacgacaa gcgctgccaa cagccttctg aaatttttgg aagagccgca tccggggacg 420
gtggcgggat tgctgactga gcaataccac cgctgctag ggacgatcgt ttcccgtgt 480
caagtgcctt cgttccggcc gttgccggcc gcagagctcg cccagggact tgtcgaggag 540
cacgtgccgt tgccgttggc gctgttggtt gccatttga caaacagctt cgaggaagca 600
ctggcgcttg ccaaagatag ttggtttgcc gaggcgcgaa cattagtgt acaatggtat 660
gagatgctgg gcaagccgga gctgcagctt ttgtttttca tccacgaccg cttgtttccg 720
catttttttg aaagccatca gcttgacctt ggacttg 757

```

<210> 180

<211> 252

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 180

```

Met Arg Trp Glu Gln Leu Ala Lys Arg Gln Pro Val Val Ala Lys Met
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Leu Gln Ser Gly Leu Glu Lys Gly Arg Ile Ser His Ala Tyr Leu Phe
      20             25             30

Glu Gly Gln Arg Gly Thr Gly Lys Lys Ala Ala Ser Leu Leu Ala
      35             40             45

Lys Arg Leu Phe Cys Leu Ser Pro Ile Gly Val Ser Pro Cys Leu Glu
      50             55             60

Cys Arg Asn Cys Arg Arg Ile Asp Ser Gly Asn His Pro Asp Val Arg
      65             70             75             80

```

Val Ile Gly Pro Asp Gly Gly Ser Ile Lys Lys Glu Gln Ile Glu Trp
85 90 95

Leu Gln Gln Glu Phe Ser Lys Thr Ala Val Glu Ser Asp Lys Lys Met
100 105 110

Tyr Ile Val Glu His Ala Asp Gln Met Thr Thr Ser Ala Ala Asn Ser
115 120 125

Leu Leu Lys Phe Leu Glu Glu Pro His Pro Gly Thr Val Ala Val Leu
130 135 140

Leu Thr Glu Gln Tyr His Arg Leu Leu Gly Thr Ile Val Ser Arg Cys
145 150 155 160

Gln Val Leu Ser Phe Arg Pro Leu Pro Pro Ala Glu Leu Ala Gln Gly
165 170 175

Leu Val Glu Glu His Val Pro Leu Pro Leu Ala Leu Leu Ala Ala His
180 185 190

Leu Thr Asn Ser Phe Glu Glu Ala Leu Ala Leu Ala Lys Asp Ser Trp
195 200 205

Phe Ala Glu Ala Arg Thr Leu Val Leu Gln Trp Tyr Glu Met Leu Gly
210 215 220

Lys Pro Glu Leu Gln Leu Leu Phe Phe Ile His Asp Arg Leu Phe Pro
225 230 235 240

His Phe Leu Glu Ser His Gln Leu Asp Leu Gly Leu
245 250

<210> 181

<211> 1677

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 181

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caagaacacg tgaccaagac gttgcaaagc gccctgcttc aacataaaat atcgcacgct 120
tacttatttt ccggcccgcg cggtacagga aaaacgagcg cagcgaaaat ttctcgccaag 180
gcggtcaact gtgaacaggc gccagcggcg gagccatgca atgagtgtcc agcttgccctc 240
ggcattacga atggaacggg tcccgatgtg ctggaaattg acgctgcttc caacaaccgc 300
gtcgaatgaaa ttcgtgatat ccgtgagaag gtgaaatttg cgccaacgtc ggcccgtctac 360
aaagtgtata tcatcgacga ggtgcataatg ctgtcgatcg gtgcgtttta cgcgctgttg 420
aaaacgttgg aggagccgcc gaaacacgctc attttcattt tggccacgac cgagccgcac 480

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aaaattccgg cgacgatcat ttcccgtcgc caacggttcg attttcgccg catcccgcctt 540
caggcgatcg tttcacggct aaagtacgtc gcaagcgccc aaggtgtcga ggcgtcagat 600
gaggcattgt ccgccatcgc ccgtgctgca gacgggggga tgcgcgatgc gctcagcttg 660
cttgatcaag ccatttcgtt cagcgacggg aaacttcggc tgcgacgacgt gctggcgatg 720
accgggggctg catcatttgc cgccttatcg agcttcacgc aagccatcca ccgcaaagat 780
acagcggcgg ttcttcagca cttggaaacg atgatggcgc aagggaaaga tccgcatcgt 840
ttggttgaag acttgatttt gtactatcgc gatttattgc tgtacaaaac cgctccctat 900
gtggaggagg cgattcaa at tgctgtcgtt gacgaagcgt tcacttcact gtcggaaatg 960
attccggttt ccaattttata cgaggccatc gagttgctga acaaaagcca gcaagagatg 1020
aagtggacaa accaccgcgc ctttctgttg gaagtggcgc ttgtgaaact ttgccatcca 1080
tcagccgcgc ccccgctcgt gtcggcttcc gagttggaac cgttgataaa gcggattgaa 1140
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gcgcgggtga aaaaactgtc caaaccgatg aaaacggggg gatataaagc cccggttggc 1260
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caagagagcg agccggttgc agcgagcgcc tcagcgtttg tattaaaatt caaatacgaa 1440
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ttgtttgagc tgacaaaccg ccgctttgaa atggtagcca ttccggaggg agaatgggga 1560
aaaataagag aagagttcat ccgcaataag gacgccatgg tggaaaaaag cgaagaagat 1620
ccgttaatcg ccgaagcgaa gcggctgttt ggcaagagc tgatcgaaat taaagaa 1677

```

<210> 182

<211> 559

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 182

```

Val Ala Tyr Gln Ala Leu Tyr Arg Val Phe Arg Pro Gln Arg Phe Ala
  1             5             10             15

Asp Met Val Gly Gln Glu His Val Thr Lys Thr Leu Gln Ser Ala Leu
      20             25             30

Leu Gln His Lys Ile Ser His Ala Tyr Leu Phe Ser Gly Pro Arg Gly
      35             40             45

Thr Gly Lys Thr Ser Ala Ala Lys Ile Phe Ala Lys Ala Val Asn Cys
      50             55             60

Glu Gln Ala Pro Ala Ala Glu Pro Cys Asn Glu Cys Pro Ala Cys Leu
      65             70             75             80

Gly Ile Thr Asn Gly Thr Val Pro Asp Val Leu Glu Ile Asp Ala Ala
      85             90             95

Ser Asn Asn Arg Val Asp Glu Ile Arg Asp Ile Arg Glu Lys Val Lys
      100            105            110

```

Phe	Ala	Pro	Thr	Ser	Ala	Arg	Tyr	Lys	Val	Tyr	Ile	Ile	Asp	Glu	Val	115	120	125	
His	Met	Leu	Ser	Ile	Gly	Ala	Phe	Asn	Ala	Leu	Leu	Lys	Thr	Leu	Glu	130	135	140	
Glu	Pro	Pro	Lys	His	Val	Ile	Phe	Ile	Leu	Ala	Thr	Thr	Glu	Pro	His	145	150	155	160
Lys	Ile	Pro	Ala	Thr	Ile	Ile	Ser	Arg	Cys	Gln	Arg	Phe	Asp	Phe	Arg	165	170	175	
Arg	Ile	Pro	Leu	Gln	Ala	Ile	Val	Ser	Arg	Leu	Lys	Tyr	Val	Ala	Ser	180	185	190	
Ala	Gln	Gly	Val	Glu	Ala	Ser	Asp	Glu	Ala	Leu	Ser	Ala	Ile	Ala	Arg	195	200	205	
Ala	Ala	Asp	Gly	Gly	Met	Arg	Asp	Ala	Leu	Ser	Leu	Leu	Asp	Gln	Ala	210	215	220	
Ile	Ser	Phe	Ser	Asp	Gly	Lys	Leu	Arg	Leu	Asp	Asp	Val	Leu	Ala	Met	225	230	235	240
Thr	Gly	Ala	Ala	Ser	Phe	Ala	Ala	Leu	Ser	Ser	Phe	Ile	Glu	Ala	Ile	245	250	255	
His	Arg	Lys	Asp	Thr	Ala	Ala	Val	Leu	Gln	His	Leu	Glu	Thr	Met	Met	260	265	270	
Ala	Gln	Gly	Lys	Asp	Pro	His	Arg	Leu	Val	Glu	Asp	Leu	Ile	Leu	Tyr	275	280	285	
Tyr	Arg	Asp	Leu	Leu	Leu	Tyr	Lys	Thr	Ala	Pro	Tyr	Val	Glu	Gly	Ala	290	295	300	
Ile	Gln	Ile	Ala	Val	Val	Asp	Glu	Ala	Phe	Thr	Ser	Leu	Ser	Glu	Met	305	310	315	320
Ile	Pro	Val	Ser	Asn	Leu	Tyr	Glu	Ala	Ile	Glu	Leu	Leu	Asn	Lys	Ser	325	330	335	
Gln	Gln	Glu	Met	Lys	Trp	Thr	Asn	His	Pro	Arg	Leu	Leu	Leu	Glu	Val	340	345	350	
Ala	Leu	Val	Lys	Leu	Cys	His	Pro	Ser	Ala	Ala	Ala	Pro	Ser	Leu	Ser	355	360	365	

Ala Ser Glu Leu Glu Pro Leu Ile Lys Arg Ile Glu Thr Leu Glu Ala
 370 375 380

Glu Leu Arg Arg Leu Lys Glu Gln Pro Pro Ala Pro Pro Ser Thr Ala
 385 390 395 400

Ala Pro Val Lys Lys Leu Ser Lys Pro Met Lys Thr Gly Gly Tyr Lys
 405 410 415

Ala Pro Val Gly Arg Ile Tyr Glu Leu Leu Lys Gln Ala Thr His Glu
 420 425 430

Asp Leu Ala Leu Val Lys Gly Cys Trp Ala Asp Val Leu Asp Thr Leu
 435 440 445

Lys Arg Gln His Lys Val Ser His Ala Ala Leu Leu Gln Glu Ser Glu
 450 455 460

Pro Val Ala Ala Ser Ala Ser Ala Phe Val Leu Lys Phe Lys Tyr Glu
 465 470 475 480

Ile His Cys Lys Met Ala Thr Asp Pro Thr Ser Ser Val Lys Glu Asn
 485 490 495

Val Glu Ala Ile Leu Phe Glu Leu Thr Asn Arg Arg Phe Glu Met Val
 500 505 510

Ala Ile Pro Glu Gly Glu Trp Gly Lys Ile Arg Glu Glu Phe Ile Arg
 515 520 525

Asn Lys Asp Ala Met Val Glu Lys Ser Glu Glu Asp Pro Leu Ile Ala
 530 535 540

Glu Ala Lys Arg Leu Phe Gly Glu Glu Leu Ile Glu Ile Lys Glu
 545 550 555

<210> 183

<211> 4301

<212> DNA

<213> Bacillus stearothermophilus

<400> 183

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 gaggagaaaa gctggcattt ttattttcag ttcgacaacg tgctgccggt tcatgtatac 180
 aaaacgtttg ccgatcggct gcagacggcg ttccgccata tcgccgccgt ccgccatacg 240

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cttgccgagc	tgcaagaagg	catgtcgccg	cttgtcgatt	ggctcagccg	gcagacgcct	360
gagctgaaag	gaaacaagct	gcttgtcggt	gcccgccatg	aagcggaagc	gctggcgatc	420
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cagcttgacg	tcagcgtcga	gccgtccaag	caagaaatgg	aacagttttt	ggcgcaaaaa	540
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aaggccgcgt	ctgcgcgcgc	gtccgggtccg	cttgtcatcg	gctatccgat	ccgcgacgag	660
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gaacggcaag	atacggcgcc	ggaaggggaa	aagagggtcg	agctccattt	gcataccccg	1020
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<210> 184

<211> 1433

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 184

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Met Val Thr Lys Glu Gln Lys Glu Arg Phe Leu Ile Leu Leu Glu Gln
 1             5             10             15

Leu Lys Met Thr Ser Asp Glu Trp Met Pro His Phe Arg Glu Ala Ala
      20             25             30

Ile Arg Lys Val Val Ile Asp Lys Glu Glu Lys Ser Trp His Phe Tyr
      35             40             45

Phe Gln Phe Asp Asn Val Leu Pro Val His Val Tyr Lys Thr Phe Ala
      50             55             60

Asp Arg Leu Gln Thr Ala Phe Arg His Ile Ala Ala Val Arg His Thr
      65             70             75             80

Met Glu Val Glu Ala Pro Arg Val Thr Glu Ala Asp Val Gln Ala Tyr
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Trp Pro Leu Cys Leu Ala Glu Leu Gln Glu Gly Met Ser Pro Leu Val
      100            105            110

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Asp	His	Ala	Val	Val	Gln	Ser	Phe	Pro	Glu	Ala	Tyr	Ser	Ala	Ala	Lys	370	375	380	
Lys	His	Gly	Met	Lys	Val	Ile	Tyr	Gly	Leu	Glu	Ala	Asn	Ile	Val	Asp	385	390	395	400
Asp	Gly	Val	Pro	Ile	Ala	Tyr	Asn	Glu	Thr	His	Arg	Arg	Leu	Ser	Glu	405	410	415	
Glu	Thr	Tyr	Val	Val	Phe	Asp	Val	Glu	Thr	Thr	Gly	Leu	Ser	Ala	Val	420	425	430	
Tyr	Asn	Thr	Ile	Ile	Glu	Leu	Ala	Ala	Val	Lys	Val	Lys	Asp	Gly	Glu	435	440	445	
Ile	Ile	Asp	Arg	Phe	Met	Ser	Phe	Ala	Asn	Pro	Gly	His	Pro	Leu	Ser	450	455	460	
Val	Thr	Thr	Met	Glu	Leu	Thr	Gly	Ile	Thr	Asp	Glu	Met	Val	Lys	Asp	465	470	475	480
Ala	Pro	Lys	Pro	Asp	Glu	Val	Leu	Ala	Arg	Phe	Val	Asp	Trp	Ala	Gly	485	490	495	
Asp	Ala	Thr	Leu	Val	Ala	His	Asn	Ala	Ser	Phe	Asp	Ile	Gly	Phe	Leu	500	505	510	
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Ile	Asp	Thr	Leu	Glu	Leu	Ala	Arg	Phe	Leu	Tyr	Pro	Asp	Leu	Lys	Asn	530	535	540	
His	Arg	Leu	Asn	Thr	Leu	Cys	Lys	Lys	Phe	Asp	Ile	Glu	Leu	Thr	Gln	545	550	555	560
His	His	Arg	Ala	Ile	Tyr	Asp	Ala	Glu	Ala	Thr	Gly	His	Leu	Leu	Met	565	570	575	
Arg	Leu	Leu	Lys	Glu	Ala	Glu	Glu	Arg	Gly	Ile	Leu	Phe	His	Asp	Glu	580	585	590	
Leu	Asn	Ser	Arg	Thr	His	Ser	Glu	Ala	Ser	Tyr	Arg	Leu	Ala	Arg	Pro	595	600	605	
Phe	His	Val	Thr	Leu	Leu	Ala	Gln	Asn	Glu	Thr	Gly	Leu	Lys	Asn	Leu	610	615	620	

Phe	Lys	Leu	Val	Ser	Leu	Ser	His	Ile	Gln	Tyr	Phe	His	Arg	Val	Pro	625	630	635	640
Arg	Ile	Pro	Arg	Ser	Val	Leu	Val	Lys	His	Arg	Asp	Gly	Leu	Leu	Val	645	650	655	
Gly	Ser	Gly	Cys	Asp	Lys	Gly	Glu	Leu	Phe	Asp	Asn	Leu	Ile	Gln	Lys	660	665	670	
Ala	Pro	Glu	Glu	Val	Glu	Asp	Ile	Ala	Arg	Phe	Tyr	Asp	Phe	Leu	Glu	675	680	685	
Val	His	Pro	Pro	Asp	Val	Tyr	Lys	Pro	Leu	Ile	Glu	Met	Asp	Tyr	Val	690	695	700	
Lys	Asp	Glu	Glu	Met	Ile	Lys	Asn	Ile	Ile	Arg	Ser	Ile	Val	Ala	Leu	705	710	715	720
Gly	Glu	Lys	Leu	Asp	Ile	Pro	Val	Val	Ala	Thr	Gly	Asn	Val	His	Tyr	725	730	735	
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Lys	Ala	Lys	Glu	Ile	Val	Val	Asp	Asn	Thr	Gln	Lys	Ile	Ala	Ser	Leu	785	790	795	800
Ile	Gly	Asp	Val	Lys	Pro	Ile	Lys	Asp	Glu	Leu	Tyr	Thr	Pro	Arg	Ile	805	810	815	
Glu	Gly	Ala	Asp	Glu	Glu	Ile	Arg	Glu	Met	Ser	Tyr	Arg	Arg	Ala	Lys	820	825	830	
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Lys	Glu	Leu	Lys	Ser	Ile	Ile	Gly	His	Gly	Phe	Ala	Val	Ile	Tyr	Leu	850	855	860	
Ile	Ser	His	Lys	Leu	Val	Lys	Lys	Ser	Leu	Asp	Asp	Gly	Tyr	Leu	Val	865	870	875	880

Gly	Ser	Arg	Gly	Ser	Val	Gly	Ser	Ser	Phe	Val	Ala	Thr	Met	Thr	Glu			
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Lys	His	Ser	Glu	Phe	Phe	Asn	Asp	Gly	Ser	Val	Gly	Ser	Gly	Phe	Asp			
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Leu	Pro	Asp	Lys	Asn	Cys	Pro	Arg	Cys	Gly	Thr	Lys	Tyr	Lys	Lys	Asp			
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945					950					955					960			
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His	Asn	Tyr	Thr	Lys	Val	Leu	Phe	Gly	Glu	Asp	Asn	Val	Tyr	Arg	Ala			
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Gly	Thr	Ile	Gly	Thr	Val	Ala	Asp	Lys	Thr	Ala	Tyr	Gly	Phe	Val	Lys			
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Ala	Tyr	Ala	Ser	Asp	His	Asn	Leu	Glu	Leu	Arg	Gly	Ala	Glu	Ile	Asp			
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Gly	Gly	Ile	Ile	Val	Val	Pro	Asp	Tyr	Met	Glu	Ile	Tyr	Asp	Phe	Thr			
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Pro	Ile	Gln	Tyr	Pro	Ala	Asp	Asp	Thr	Ser	Ser	Glu	Trp	Arg	Thr	Thr			
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His	Phe	Asp	Phe	His	Ser	Ile	His	Asp	Asn	Leu	Leu	Lys	Leu	Asp	Ile			
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Leu	Gly	His	Asp	Asp	Pro	Thr	Val	Ile	Arg	Met	Leu	Gln	Asp	Leu	Ser			
	1090					1095				1100								
Gly	Ile	Asp	Pro	Lys	Thr	Ile	Pro	Thr	Asp	Asp	Pro	Asp	Val	Met	Gly			
1105				1110					1115					1120				
Ile	Phe	Ser	Ser	Thr	Glu	Pro	Leu	Gly	Val	Thr	Pro	Glu	Gln	Ile	Met			
				1125				1130					1135					

Cys	Asn	Val	Gly	Thr	Ile	Gly	Ile	Pro	Glu	Phe	Gly	Thr	Arg	Phe	Val			
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Arg	Gln	Met	Leu	Glu	Glu	Thr	Arg	Pro	Lys	Thr	Phe	Ser	Glu	Leu	Val			
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Gln	Glu	Leu	Ile	Gln	Asn	Gly	Thr	Cys	Thr	Leu	Ser	Glu	Val	Ile	Gly			
1185					1190				1195					1200				
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Thr	Pro	Glu	Phe	Glu	Ala	Glu	Met	Arg	Lys	His	Asp	Val	Pro	Glu	Trp			
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Tyr	Ile	Asp	Ser	Cys	Lys	Lys	Ile	Lys	Tyr	Met	Phe	Pro	Lys	Ala	His			
	1250					1255					1260							
Ala	Ala	Ala	Tyr	Val	Leu	Met	Ala	Val	Arg	Ile	Ala	Tyr	Phe	Lys	Val			
1265					1270					1275				1280				
His	His	Pro	Leu	Leu	Tyr	Tyr	Ala	Ser	Tyr	Phe	Thr	Val	Arg	Ala	Glu			
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Asp	Phe	Asp	Leu	Asp	Ala	Met	Ile	Lys	Gly	Ser	Pro	Ala	Ile	Arg	Lys			
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Arg	Ile	Glu	Glu	Ile	Asn	Ala	Lys	Gly	Ile	Gln	Ala	Thr	Ala	Lys	Glu			
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Lys	Ser	Leu	Leu	Thr	Val	Leu	Glu	Val	Ala	Leu	Glu	Met	Cys	Glu	Arg			
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Phe	Val	Ile	Asp	Gly	Asn	Ser	Leu	Ile	Pro	Pro	Phe	Asn	Ala	Ile	Pro			
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Gly	Leu	Gly	Thr	Asn	Val	Ala	Gln	Ala	Ile	Val	Arg	Ala	Arg	Glu	Glu			
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Gly Glu Phe Leu Ser Lys Glu Asp Leu Gln Gln Arg Gly Lys Leu Ser
 1395 1400 1405

Lys Thr Leu Leu Glu Tyr Leu Glu Ser Arg Gly Cys Leu Asp Ser Leu
 1410 1415 1420

Pro Asp His Asn Gln Leu Ser Leu Phe
 1425 1430

<210> 185
 <211> 199
 <212> PRT
 <213> Thermus thermophilus

<400> 185
 Thr Pro Lys Gly Lys Asp Leu Val Arg His Leu Glu Asn Arg Ala Lys
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 20 25 30

Leu Glu Gly Asp Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala
 35 40 45

Leu Leu Ser Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala
 50 55 60

Leu Arg Pro Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu
 65 70 75 80

Lys Asp Pro Lys Glu Ala Leu Leu Arg Leu Gly Arg Leu Lys Glu Glu
 85 90 95

Gly Glu Glu Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala
 100 105 110

Leu Leu Ala Arg Ala Phe Phe Leu Leu Arg Glu Met Pro Arg Pro Lys
 115 120 125

Glu Glu Asp Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys
 130 135 140

Ala Leu Leu Glu Ala Ala Arg Arg Leu Thr Glu Glu Ala Leu Lys Glu
 145 150 155 160

Ala Leu Asp Ala Leu Met Glu Ala Glu Lys Arg Ala Lys Gly Gly Lys

165

170

175

Asp Pro Trp Leu Ala Leu Glu Ala Ala Val Leu Arg Leu Ala Arg Pro
 180 - - - - - 185 . - - - 190 - - - - -

Ala Gly Gln Pro Arg Val Asp
 195

<210> 186

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 186

gcccagtacc tcgcctccct cgagggg

27

<210> 187

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 187

ggcccccttg gccttctcgg cctccat

27

<210> 188

<211> 331

<212> DNA

<213> Thermus thermophilus

<400> 188

agactcgagg ccctggagcg ggagctggag aagcttgccc tcctctcccc acccctcacc 60
 ctggagaagg tggagaagggt ggtggccctg agggcccccc tcacgggctt tgacctggtg 120
 cgctccgtcc tggagaagga cccaaggag gccctcctgc gcctcaggcg cctcaggagg 180
 gagggggagg agcccctcag gctcctcggg gccctctcct ggcagttcgc cctcctcgcc 240
 cgggccttct tcctcctcgg ggaaaacccc agggccaagg aggaggacct cgcccgcctc 300
 gaggcccacc cctacgccgc caagaaggcc a 331

<210> 189

160

<211> 110
<212> PRT
<213> Thermus thermophilus

<400> 189

Arg Leu Glu Ala Leu Glu Arg Glu Leu Glu Lys Leu Ala Leu Leu Ser
1 5 10 15

Pro Pro Leu Thr Leu Glu Lys Val Glu Lys Val Val Ala Leu Arg Pro
20 25 30

Pro Leu Thr Gly Phe Asp Leu Val Arg Ser Val Leu Glu Lys Asp Pro
35 40 45

Lys Glu Ala Leu Leu Arg Leu Arg Arg Leu Arg Glu Glu Gly Glu Glu
50 55 60

Pro Leu Arg Leu Leu Gly Ala Leu Ser Trp Gln Phe Ala Leu Leu Ala
65 70 75 80

Arg Ala Phe Phe Leu Leu Arg Glu Asn Pro Arg Pro Lys Glu Glu Asp
85 90 95

Leu Ala Arg Leu Glu Ala His Pro Tyr Ala Ala Lys Lys Ala
100 105 110

<210> 190
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 190
gtggtgtcta gacatcataa cggttctggc a

31

<210> 191
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer

<400> 191

gagggccacc accttctcca ctttctc

27

<210> 192

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 192

ctccgtcctg gagaaggacc ccaag

25

<210> 193

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<220>

<221> primer_bind

<222> (15)

<223> S at position 15 can be either C or G

<220>

<221> primer_bind

<222> (27)

<223> S at position 27 can be either C or G

<400> 193

cgcggaattca acgcsctcct caagacsct

29

<210> 194

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 194

gacacttaac atatggtcat cgccttcacc g

31

<210> 195
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: PCR primer

 <400> 195
 gtgtgtgaat tcgggtcaac gggcgaggcg gaggaccg 38

 <210> 196
 <211> 10
 <212> PRT
 <213> *Deinococcus radiodurans*

 <400> 196
 Val Ile Leu Asn Pro Gly Ser Val Gly Gln
 1 5 10

 <210> 197
 <211> 10
 <212> PRT
 <213> *Methanococcus jannaschii*

 <400> 197
 Tyr Leu Ile Asn Pro Gly Ser Val Gly Gln
 1 5 10

 <210> 198
 <211> 10
 <212> PRT
 <213> *Thermotoga maritima*

 <400> 198
 Leu Val Leu Asn Pro Gly Ser Ala Gly Arg
 1 5 10

 <210> 199
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 199
ctggtgaacc cgggctccgt gggccagc

28

<210> 200
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 200
Leu Leu Val Asn Pro Gly Ser Val Gly Gln
1 5 10

<210> 201
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR primer

<400> 201
ctcaggagc ttgaggagg tggtggc

27

<210> 202
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: polypeptide

<400> 202
Ala Asn Thr Leu Leu Lys Leu Leu Glu
1 5

<210> 203
<211> 32
<212> PRT

<213> *Deinococcus radiodurans*

<400> 203

Gly Phe Gly Gly Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Leu Ser Pro Arg His Asn Val Arg Glu Asp Glu Tyr Gly Gly
20 25 30

<210> 204

<211> 32

<212> PRT

<213> *Caenorhabditis elegans*

<400> 204

Gly Phe Asp Gly Ile Gln Leu His Gly Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Thr Ser Pro Thr Thr Asn Lys Arg Val Asp Lys Tyr Gly Gly
20 25 30

<210> 205

<211> 32

<212> PRT

<213> *Pseudomonas aeruginosa*

<400> 205

Gly Phe Ser Gly Val Glu Ile His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Gln Phe Leu Ser Pro Leu Ser Asn Arg Arg Ser Asp Ala Trp Gly Gly
20 25 30

<210> 206

<211> 32

<212> PRT

<213> Archaeoglobus fulgidus

<400> 206

Gly Phe Asp Ala Val Gln Leu His Ala Ala His Gly Tyr Leu Leu Ser
1 5 10 15

Glu Phe Ile Ser Pro His Val Asn Arg Arg Lys Asp Glu Tyr Gly Gly
20 25 30

<210> 207

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 207

catcctggac tcggcccacc tcctcaccga 30

<210> 208

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: polypeptide

<400> 208

Ile Leu Asp Ser Ala His Leu Leu Thr
1 5

<210> 209

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 209

gaggaggtag ccgtgggccc cgaggagctc cac 33

<210> 210

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: polypeptide

<400> 210

Val Glu Leu His Ala Ala His Gly Tyr Leu Leu

1

5

10

<210> 211

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 211

ggctttccca tatggctcta caccggctc ac

32

<210> 212

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR primer

<400> 212

gcgtggatcc acggtcatgt ctctaagtc

29